



## SUBSTITUTE SEQUENCE LISTING

<110> Lu, Peter  
Garman, Jonathan David  
Candia III, Albert Frederick  
Arbor Vita Corporation

<120> CLASP-7 Transmembrane Protein

<130> 020054-000611US

<140> US 09/736,968

<141> 2000-12-13

<150> US 60/160,860

<151> 1999-10-21

<150> US 60/162,498

<151> 1999-10-29

<150> US 60/170,453

<151> 1999-12-13

<150> US 60/176,195

<151> 2000-01-14

<150> US 60/182,296

<151> 2000-02-14

<150> US 09/547,276

<151> 2000-04-11

<150> US 60/196,267

<151> 2000-04-11

<150> US 60/196,460

<151> 2000-04-11

<150> US 60/196,527

<151> 2000-04-11

<150> US 60/196,528

<151> 2000-04-11

<150> US 09/687,837

<151> 2000-10-13

<150> US 60/240,503

<151> 2000-10-13

<150> US 60/240,508

<151> 2000-10-13

<150> US 60/240,539

<151> 2000-10-13

<150> US 60/240,543

<151> 2000-10-13

<160> 115

RECEIVED  
APR 05 2002  
TECH CENTER 1600/2900

B1

<170> PatentIn Ver. 2.1

<210> 1

<211> 6372

<212> DNA

<213> Homo sapiens

<220>

<223> full length human CLASP-7 cDNA

<220>

<221> CDS

<222> (13)..(6156)

<223> human CLASP-7

<400> 1

```

gacgcgagga cc atg gct gcc tcc gag cgc cgc gcc ttc gcg cac aag atc 51
      Met Ala Ala Ser Glu Arg Arg Ala Phe Ala His Lys Ile
              1              5              10

aac agg acg gtg gcc gca gag gtg cgg aag cag gtg tcc cgg gaa cgc 99
Asn Arg Thr Val Ala Ala Glu Val Arg Lys Gln Val Ser Arg Glu Arg
      15              20              25

agt ggc tcc ccc cac tcc agc agg cgc tgc agc agc tcc ctg ggg gtc 147
Ser Gly Ser Pro His Ser Ser Arg Arg Cys Ser Ser Ser Leu Gly Val
      30              35              40              45

cca ctg act gaa gtt gtc gag ccc ctg gac ttt gag gat gta ctt ctg 195
Pro Leu Thr Glu Val Val Glu Pro Leu Asp Phe Glu Asp Val Leu Leu
              50              55              60

agc cgg cca cca gat gct gag ccc ggg ccc ctc agg gac ctg gta gaa 243
Ser Arg Pro Pro Asp Ala Glu Pro Gly Pro Leu Arg Asp Leu Val Glu
              65              70              75

ttc cca gct gat gac ttg gag ctg ctg ctg cag ccc cgg gaa tgc cgg 291
Phe Pro Ala Asp Asp Leu Glu Leu Leu Leu Gln Pro Arg Glu Cys Arg
      80              85              90

acc acg gag ccc ggg atc ccc aag gat gaa aaa ctg gat gcc cag gtg 339
Thr Thr Glu Pro Gly Ile Pro Lys Asp Glu Lys Leu Asp Ala Gln Val
      95              100              105

agg gcc gcg gtg gag atg tat att gag gac tgg gtc att gtc cac aga 387
Arg Ala Ala Val Glu Met Tyr Ile Glu Asp Trp Val Ile Val His Arg
     110              115              120              125

agg tat cag tac ctg agt gca gca tac agc ccc gtc acc aca gac aca 435
Arg Tyr Gln Tyr Leu Ser Ala Ala Tyr Ser Pro Val Thr Thr Asp Thr
              130              135              140

cag cgg gag cga cag aag ggc ctc ccc cgc cag gtc ttt gag cag gat 483
Gln Arg Glu Arg Gln Lys Gly Leu Pro Arg Gln Val Phe Glu Gln Asp
              145              150              155

gct tct gga gac gag agg tcc ggc cct gag gac tcg aat gac tcc cgg 531
Ala Ser Gly Asp Glu Arg Ser Gly Pro Glu Asp Ser Asn Asp Ser Arg
              160              165              170

cgt ggc tcg ggc tcc ccg gaa gac acc cct cga agc agt ggt gcc tct 579

```

Arg	Gly	Ser	Gly	Ser	Pro	Glu	Asp	Thr	Pro	Arg	Ser	Ser	Gly	Ala	Ser		
175						180					185						
agc	atc	ttc	gac	ctg	agg	aac	ctg	gca	gct	gac	tca	ttg	ctg	ccc	tct	627	
Ser	Ile	Phe	Asp	Leu	Arg	Asn	Leu	Ala	Ala	Asp	Ser	Leu	Leu	Pro	Ser		
190					195					200					205		
ctg	cta	gag	cgg	gcg	gcc	cca	gaa	gat	gtg	gac	cgg	cgc	aat	gaa	acc	675	
Leu	Leu	Glu	Arg	Ala	Ala	Pro	Glu	Asp	Val	Asp	Arg	Arg	Asn	Glu	Thr		
				210					215					220			
ctt	cga	cgg	cag	cac	cgg	ccc	ccg	gcc	ctg	ctc	acc	ctc	tac	ccg	gca	723	
Leu	Arg	Arg	Gln	His	Arg	Pro	Pro	Ala	Leu	Leu	Thr	Leu	Tyr	Pro	Ala		
			225					230					235				
cct	gac	gag	gat	gaa	gcc	gtg	gaa	cgc	tgt	agc	cgc	cca	gag	cca	ccc	771	
Pro	Asp	Glu	Asp	Glu	Ala	Val	Glu	Arg	Cys	Ser	Arg	Pro	Glu	Pro	Pro		
		240					245				250						
cgc	gag	cac	ttt	gga	caa	agg	atc	ttg	gtc	aag	tgt	ctg	tcg	ctc	aag	819	
Arg	Glu	His	Phe	Gly	Gln	Arg	Ile	Leu	Val	Lys	Cys	Leu	Ser	Leu	Lys		
	255					260					265						
ttc	gag	att	gaa	att	gag	ccc	atc	ttt	ggg	atc	ttg	gct	ctg	tat	gat	867	
Phe	Glu	Ile	Glu	Ile	Glu	Pro	Ile	Phe	Gly	Ile	Leu	Ala	Leu	Tyr	Asp		
270					275				280						285		
gtg	cgg	gag	aaa	aag	aag	atc	tcg	gag	aac	ttc	tac	ttc	gac	ctg	aac	915	
Val	Arg	Glu	Lys	Lys	Lys	Ile	Ser	Glu	Asn	Phe	Tyr	Phe	Asp	Leu	Asn		
				290					295					300			
tcg	gac	tcc	atg	aag	ggg	ctg	ctt	cgg	gct	cat	ggc	acc	cac	cct	gcc	963	
Ser	Asp	Ser	Met	Lys	Gly	Leu	Leu	Arg	Ala	His	Gly	Thr	His	Pro	Ala		
			305					310					315				
atc	tcc	acc	ctg	gcc	cgc	tct	gcc	atc	ttc	tct	gtg	acc	tac	ccc	tca	1011	
Ile	Ser	Thr	Leu	Ala	Arg	Ser	Ala	Ile	Phe	Ser	Val	Thr	Tyr	Pro	Ser		
		320					325					330					
cct	gac	atc	ttc	ctg	gtc	atc	aag	ttg	gag	aag	gtg	ctt	cag	caa	ggg	1059	
Pro	Asp	Ile	Phe	Leu	Val	Ile	Lys	Leu	Glu	Lys	Val	Leu	Gln	Gln	Gly		
	335					340					345						
gac	atc	agt	gag	tgc	tgt	gag	cct	tac	atg	gtg	ttg	aaa	gaa	gtg	gac	1107	
Asp	Ile	Ser	Glu	Cys	Cys	Glu	Pro	Tyr	Met	Val	Leu	Lys	Glu	Val	Asp		
350				355					360						365		
aca	gcc	aag	aac	aaa	gag	aag	cta	gag	aag	ctg	cgc	ctg	gcg	gcc	gag	1155	
Thr	Ala	Lys	Asn	Lys	Glu	Lys	Leu	Glu	Lys	Leu	Arg	Leu	Ala	Ala	Glu		
			370					375					380				
cag	ttc	tgc	acc	cgc	ctg	ggc	cgc	tac	cgc	atg	ccc	ttc	gcc	tgg	acg	1203	
Gln	Phe	Cys	Thr	Arg	Leu	Gly	Arg	Tyr	Arg	Met	Pro	Phe	Ala	Trp	Thr		
			385					390					395				
gcc	gtg	cac	ttg	gcc	aac	atc	gtg	agc	agc	gct	ggg	cag	ctg	gac	cgg	1251	
Ala	Val	His	Leu	Ala	Asn	Ile	Val	Ser	Ser	Ala	Gly	Gln	Leu	Asp	Arg		
		400					405					410					
gac	tct	gac	tcg	gag	ggc	gag	cgc	cgg	cca	gcc	tgg	aca	gac	cgc	cgc	1299	
Asp	Ser	Asp	Ser	Glu	Gly	Glu	Arg	Arg	Pro	Ala	Trp	Thr	Asp	Arg	Arg		

415				420				425								
cgt Arg 430	cgg Arg	ggg Gly	ccc Pro	cag Gln	gac Asp	cgg Arg	gcg Ala	agt Ser	agt Ser	ggg Gly	gac Asp	gac Asp	gcc Ala	tgc Cys	agc Ser	1347
				435				440				445				
ttc Phe	tct Ser	ggc Gly	ttc Phe	cgt Arg 450	cca Pro	gcc Ala	acg Thr	cta Leu	act Thr 455	gtc Val	aca Thr	aac Asn	ttc Phe	ttt Phe 460	aag Lys	1395
				465				470				475				
cag Gln	gag Glu	gct Ala	gag Glu 465	cga Arg	ctc Leu	agt Ser	gac Asp	gag Glu	gac Asp	ctc Leu	ttc Phe	aag Lys	ttc Phe 475	ctg Leu	gct Ala	1443
				480				485				490				
gac Asp	atg Met	agg Arg 480	cgc Arg	ccg Pro	tcg Ser	tcc Ser	ctg Leu 485	ctg Leu	cgg Arg	cga Arg	cta Leu	cgt Arg 490	cct Pro	gtg Val	act Thr	1491
				495				500				505				
gcc Ala 495	cag Gln	ctc Leu	aag Lys	atc Ile	gac Asp	att Ile 500	tct Ser	ccg Pro	gct Ala	cct Pro	gaa Glu 505	aat Asn	ccc Pro	cac His	ttc Phe	1539
				510				515				520				
tgc Cys 510	ctc Leu	tcc Ser	cct Pro	gag Glu 515	ctg Leu	ctt Leu	cat His	atc Ile	aag Lys	ccc Pro 520	tac Tyr	ccg Pro	gac Asp	ccc Pro	agg Arg 525	1587
				530				535				540				
ggc Gly	cgg Arg	ccc Pro	acc Thr	aag Lys 530	gag Glu	att Ile	ctg Leu	gag Glu	ttc Phe 535	ccc Pro	gcc Ala	cgc Arg	gaa Glu	gtc Val 540	tat Tyr	1635
				545				550				555				
gcc Ala	ccc Pro	cat His	acc Thr 545	agc Ser	tac Tyr	agg Arg	aac Asn	ctg Leu 550	ctg Leu	tac Tyr	gtg Val	tac Tyr	ccg Pro 555	cac His	agc Ser	1683
				560				565				570				
ctc Leu	aac Asn	ttc Phe 560	agc Ser	agc Ser	cgc Arg	cag Gln	ggc Gly 565	tcc Ser	gtg Val	cgc Arg	aac Asn	ctt Leu 570	gct Ala	gtg Val	cga Arg	1731
				575				580				585				
gtg Val 575	cag Gln	tac Tyr	atg Met	aca Thr	ggc Gly	gag Glu 580	gac Asp	ccc Pro	agc Ser	cag Gln	gct Ala 585	ctg Leu	ccg Pro	gtc Val	atc Ile	1779
				590				595				600				
ttt Phe 590	ggc Gly	aag Lys	tcc Ser	agc Ser	tgc Cys 595	agt Ser	gaa Glu	ttt Phe	acc Thr	cgc Arg 600	gag Glu	gcc Ala	ttc Phe	aca Thr	ccg Pro 605	1827
				610				615				620				
gtg Val	gtc Val	tac Tyr	cat His	aac Asn 610	aag Lys	tcc Ser	ccc Pro	gag Glu	ttc Phe 615	tac Tyr	gag Glu	gag Glu	ttc Phe	aag Lys 620	ctg Leu	1875
				625				630				635				
cat His	ctt Leu	cca Pro	gcc Ala 625	tgc Cys	gtg Val	aca Thr	gag Glu	aac Asn 630	cat His	cac His	ctg Leu	ctg Leu	ttc Phe 635	acc Thr	ttc Phe	1923
				640				645				650				
tac Tyr	cat His	gtc Val 640	agc Ser	tgc Cys	cag Gln	ccc Pro	cgg Arg 645	ccg Pro	ggc Gly	act Thr	gcc Ala	ctg Leu 650	gag Glu	aca Thr	ccc Pro	1971
				655				660				665				
gtg Val 655	ggc Gly	ttt Phe	act Thr	tgg Trp	atc Ile	cca Pro 660	ctg Leu	ctg Leu	cag Gln	cac His	ggg Gly 665	cgc Arg	ctg Leu	agg Arg	acc Thr	2019

ggc ccc ttc tgt ctc cca gtg tct gtg gac cag ccg ccg ccc agc tat	2067
Gly Pro Phe Cys Leu Pro Val Ser Val Asp Gln Pro Pro Pro Ser Tyr	
670 675 680 685	
tcc gtg ctc aca ccc gat gtg gcg ctt ccg ggc atg cgc tgg gtg gac	2115
Ser Val Leu Thr Pro Asp Val Ala Leu Pro Gly Met Arg Trp Val Asp	
690 695 700	
ggt cac aag ggc gtg ttc agt gtg gag ctc aca gcc gtg tcc tct gtg	2163
Gly His Lys Gly Val Phe Ser Val Glu Leu Thr Ala Val Ser Ser Val	
705 710 715	
cac ccc cag gac ccc tac ctg gac aaa ttc ttc acc ctg gtg cac gtc	2211
His Pro Gln Asp Pro Tyr Leu Asp Lys Phe Phe Thr Leu Val His Val	
720 725 730	
ctg gag gag gga gcc ttc cca ttc cgg ctc aag gac act gtg ctg agc	2259
Leu Glu Glu Gly Ala Phe Pro Phe Arg Leu Lys Asp Thr Val Leu Ser	
735 740 745	
gag ggc aac gtg gag cag gag ctg cgg gcc agt ctt gca gca ctg cgc	2307
Glu Gly Asn Val Glu Gln Glu Leu Arg Ala Ser Leu Ala Ala Leu Arg	
750 755 760 765	
ctg gcc agc ccc gaa ccc ctt gtg gcc ttc tcc cac cac gtg ctg gac	2355
Leu Ala Ser Pro Glu Pro Leu Val Ala Phe Ser His His Val Leu Asp	
770 775 780	
aag ctc gtg cgt ctg gtc atc agg ccc ccg atc atc agt ggc cag att	2403
Lys Leu Val Arg Leu Val Ile Arg Pro Pro Ile Ile Ser Gly Gln Ile	
785 790 795	
gtg aac ctg ggc cgt gga gcc ttt gaa gca atg gcc cat gta gtc agc	2451
Val Asn Leu Gly Arg Gly Ala Phe Glu Ala Met Ala His Val Val Ser	
800 805 810	
ctt gtt cac cgg agc ctg gag gca gcc cag gat gcc cgc ggt cac tgc	2499
Leu Val His Arg Ser Leu Glu Ala Ala Gln Asp Ala Arg Gly His Cys	
815 820 825	
cca cag ctg gct gcc tac gtc cac tac gcc ttt cgc ctt cct ggc act	2547
Pro Gln Leu Ala Ala Tyr Val His Tyr Ala Phe Arg Leu Pro Gly Thr	
830 835 840 845	
gag ccc agc ctc ccg gat ggg gcc cct cca gtg aca gtg cag gct gcc	2595
Glu Pro Ser Leu Pro Asp Gly Ala Pro Pro Val Thr Val Gln Ala Ala	
850 855 860	
aca ctg gcc cgt ggc tct ggt cgc ccc gca agc ctc tac ctg gcg cgt	2643
Thr Leu Ala Arg Gly Ser Gly Arg Pro Ala Ser Leu Tyr Leu Ala Arg	
865 870 875	
tcc aag agc atc agc agc agc aac cct gac ctc gcc gtg gcc cct ggc	2691
Ser Lys Ser Ile Ser Ser Ser Asn Pro Asp Leu Ala Val Ala Pro Gly	
880 885 890	
tct gtg gat gac gag gtt tcc cgc atc ctg gcc agc aag ctg ctt cac	2739
Ser Val Asp Asp Glu Val Ser Arg Ile Leu Ala Ser Lys Leu Leu His	
895 900 905	

gag gag ctg gct ctg cag tgg gtg gtc agc agc agt gcc gta cgc gag	2787
Glu Glu Leu Ala Leu Gln Trp Val Val Ser Ser Ser Ala Val Arg Glu	
910 915 920 925	
gcc atc ctc cag cac gcc tgg ttc ttc ttc cag ctc atg gtg aag agt	2835
Ala Ile Leu Gln His Ala Trp Phe Phe Phe Gln Leu Met Val Lys Ser	
930 935 940	
atg gcg ctg cac ctg ctg ctt ggc cag cga cta gac aca ccc cgc aag	2883
Met Ala Leu His Leu Leu Leu Gly Gln Arg Leu Asp Thr Pro Arg Lys	
945 950 955	
ctg cgc ttc ccc gga cgc ttc ctg gac gac atc act gcc ttg gtg ggc	2931
Leu Arg Phe Pro Gly Arg Phe Leu Asp Asp Ile Thr Ala Leu Val Gly	
960 965 970	
tct gtg ggc ctg gag gtc atc acc cgt gtc cac aag gat gtg gag ctg	2979
Ser Val Gly Leu Glu Val Ile Thr Arg Val His Lys Asp Val Glu Leu	
975 980 985	
gcc gag cac ctc aac gcc agc ctg gct ttc ttc ctc agt gac ctt ctg	3027
Ala Glu His Leu Asn Ala Ser Leu Ala Phe Phe Leu Ser Asp Leu Leu	
990 995 1000 1005	
tcc ctg gtg gac cgg ggc ttt gtc ttc agc ctg gtc cgg gcc cac tac	3075
Ser Leu Val Asp Arg Gly Phe Val Phe Ser Leu Val Arg Ala His Tyr	
1010 1015 1020	
aag cag gtg gcc acg cgg ctc cag tcg tcc cct aat cca gca gcc ctg	3123
Lys Gln Val Ala Thr Arg Leu Gln Ser Ser Pro Asn Pro Ala Ala Leu	
1025 1030 1035	
ctg acc ctg cgc atg gaa ttc acc cgc atc ctg tgc agc cac gag cac	3171
Leu Thr Leu Arg Met Glu Phe Thr Arg Ile Leu Cys Ser His Glu His	
1040 1045 1050	
tac gtg acc ctc aac ctc ccc tgc tgc ccc ctg tca cct cca gcc tcg	3219
Tyr Val Thr Leu Asn Leu Pro Cys Cys Pro Leu Ser Pro Pro Ala Ser	
1055 1060 1065	
ccc tcc ccc tct gtg tcc tcc acc acc tcc cag agc tcc acc ttc tcc	3267
Pro Ser Pro Ser Val Ser Ser Thr Thr Ser Gln Ser Ser Thr Phe Ser	
1070 1075 1080 1085	
agc caa gcc ccg gac ccc aag gtg acc agc atg ttc gaa ctg agt gga	3315
Ser Gln Ala Pro Asp Pro Lys Val Thr Ser Met Phe Glu Leu Ser Gly	
1090 1095 1100	
cca ttc cgg cag cag cac ttc cta gct ggg ctc ctg ctg acg gag ctg	3363
Pro Phe Arg Gln Gln His Phe Leu Ala Gly Leu Leu Leu Thr Glu Leu	
1105 1110 1115	
gca ctg gcc ctc gaa cct gag gct gaa ggg gca ttc ctg ttg cac aag	3411
Ala Leu Ala Leu Glu Pro Glu Ala Glu Gly Ala Phe Leu Leu His Lys	
1120 1125 1130	
aag gcc atc agt gct gtg cac agc ctg cta tgt ggc cat gac act gac	3459
Lys Ala Ile Ser Ala Val His Ser Leu Leu Cys Gly His Asp Thr Asp	
1135 1140 1145	
ccc cgc tac gcc gag gcc act gtg aag gct cgt gtg gcc gag ctg tac	3507

—

1390	1395	1400	1405	
tca gaa gcc cgg gag agc gtc ttg ggg gca gtg ctg aag gtt gtg ctg				4275
Ser Glu Ala Arg Glu Ser Val Leu Gly Ala Val Leu Lys Val Val Leu				
	1410	1415	1420	
tac agc ctg ggc agt gcc cag agt gcc ctc ttc ttg cag cat ggc ctg				4323
Tyr Ser Leu Gly Ser Ala Gln Ser Ala Leu Phe Leu Gln His Gly Leu				
	1425	1430	1435	
gcc acc cag agg gcc ctt gtg tcc aag ttc ccg gag ctg ctg ttc gag				4371
Ala Thr Gln Arg Ala Leu Val Ser Lys Phe Pro Glu Leu Leu Phe Glu				
	1440	1445	1450	
gag gac acg gag ctg tgt gcc gac ctg tgc ctg agg ctc cta cga cac				4419
Glu Asp Thr Glu Leu Cys Ala Asp Leu Cys Leu Arg Leu Leu Arg His				
	1455	1460	1465	
tgt ggc agc cgc atc agc acc atc cgc acg cac gcc agc gcc tcg ctg				4467
Cys Gly Ser Arg Ile Ser Thr Ile Arg Thr His Ala Ser Ala Ser Leu				
	1470	1475	1480	1485
tac ctg ctc atg cga cag aac ttc gag atc ggc cac aac ttt gcc cgt				4515
Tyr Leu Leu Met Arg Gln Asn Phe Glu Ile Gly His Asn Phe Ala Arg				
	1490	1495	1500	
gtg aag atg cag gtc acc atg tct ctc tcg tcc ctg gtg ggg acg acg				4563
Val Lys Met Gln Val Thr Met Ser Leu Ser Ser Leu Val Gly Thr Thr				
	1505	1510	1515	
cag aac ttc agt gaa gag cac ctg cga cgt tca ctc aaa acc atc ctc				4611
Gln Asn Phe Ser Glu Glu His Leu Arg Arg Ser Leu Lys Thr Ile Leu				
	1520	1525	1530	
acc tat gct gag gag gac atg ggg ctg cgg gac agc acc ttc gca gag				4659
Thr Tyr Ala Glu Glu Asp Met Gly Leu Arg Asp Ser Thr Phe Ala Glu				
	1535	1540	1545	
cag gtc cag gac ctg atg ttc aac ctg cac atg atc ctg acg gac acg				4707
Gln Val Gln Asp Leu Met Phe Asn Leu His Met Ile Leu Thr Asp Thr				
	1550	1555	1560	1565
gtg aag atg aag gaa cac cag gag gac cct gag atg ctc atc gac ctc				4755
Val Lys Met Lys Glu His Gln Glu Asp Pro Glu Met Leu Ile Asp Leu				
	1570	1575	1580	
atg tac aga att gcc cgg ggc tac cag ggc tca ccg gac ctt cgg ctg				4803
Met Tyr Arg Ile Ala Arg Gly Tyr Gln Gly Ser Pro Asp Leu Arg Leu				
	1585	1590	1595	
acc tgg ttg cag aac atg gcc ggg aag cac gcg gag ctg ggc aac cac				4851
Thr Trp Leu Gln Asn Met Ala Gly Lys His Ala Glu Leu Gly Asn His				
	1600	1605	1610	
gcc gag gcc gcc cag tgc atg gtg cac gcg gcc gcc ctc gtg gct gag				4899
Ala Glu Ala Ala Gln Cys Met Val His Ala Ala Ala Leu Val Ala Glu				
	1615	1620	1625	
tac ctc gcc ctg ctc gag gac cag cgc cac ctg ccc gtg ggc tgc gtt				4947
Tyr Leu Ala Leu Leu Glu Asp Gln Arg His Leu Pro Val Gly Cys Val				
	1630	1635	1640	1645



tcc ttc cag aac atc tca tcc aac gtg cta gag gag tcc gcc atc tcc Ser Phe Gln Asn Ile Ser Ser Asn Val Leu Glu Glu Ser Ala Ile Ser	4995
1650 1655 1660	
gac gac atc ctg tcg ccc gac gag gag ggc ttc tgc tcc ggg aag cac Asp Asp Ile Leu Ser Pro Asp Glu Glu Gly Phe Cys Ser Gly Lys His	5043
1665 1670 1675	
ttc act gag ctg ggg ctg gta ggg ttg ctg gaa cag gca gcc ggc tac Phe Thr Glu Leu Gly Leu Val Gly Leu Leu Glu Gln Ala Ala Gly Tyr	5091
1680 1685 1690	
ttc acc atg ggc ggg ctc tac gag gcg gtg aat gag gtc tac aag aac Phe Thr Met Gly Gly Leu Tyr Glu Ala Val Asn Glu Val Tyr Lys Asn	5139
1695 1700 1705	
ctc atc ccc atc ctg gaa gcc cac cgt gac tac aag aag ctg gcc gcg Leu Ile Pro Ile Leu Glu Ala His Arg Asp Tyr Lys Lys Leu Ala Ala	5187
1710 1715 1720 1725	
gtg cac ggc aaa ctg cag gag gcc ttc acc aag atc atg cac cag agt Val His Gly Lys Leu Gln Glu Ala Phe Thr Lys Ile Met His Gln Ser	5235
1730 1735 1740	
tcc ggc tgg gag cgc gtg ttc ggg acg tat ttc cgc gtg ggc ttc tac Ser Gly Trp Glu Arg Val Phe Gly Thr Tyr Phe Arg Val Gly Phe Tyr	5283
1745 1750 1755	
ggc gcc cac ttc ggt gac ctg gat gag cag gag ttt gtg tac aag gag Gly Ala His Phe Gly Asp Leu Asp Glu Gln Glu Phe Val Tyr Lys Glu	5331
1760 1765 1770	
cca tcg atc acg aag ctg gca gag atc tca cac cgg ctg gag gag ttc Pro Ser Ile Thr Lys Leu Ala Glu Ile Ser His Arg Leu Glu Glu Phe	5379
1775 1780 1785	
tac acg gag aga ttt ggc gac gac gtc gtt gag att atc aaa gac tct Tyr Thr Glu Arg Phe Gly Asp Asp Val Val Glu Ile Ile Lys Asp Ser	5427
1790 1795 1800 1805	
tac cct gtg gac aag tcc aag ctt gac tca caa aag gcc tac atc cag Tyr Pro Val Asp Lys Ser Lys Leu Asp Ser Gln Lys Ala Tyr Ile Gln	5475
1810 1815 1820	
atc acg tat gtg gaa ccg tac ttt gat acc tac gag ctc aag gac cgg Ile Thr Tyr Val Glu Pro Tyr Phe Asp Thr Tyr Glu Leu Lys Asp Arg	5523
1825 1830 1835	
gtg acc tac ttt gac cgc aac tat ggg ctt cgc aca ttc ctg ttc tgc Val Thr Tyr Phe Asp Arg Asn Tyr Gly Leu Arg Thr Phe Leu Phe Cys	5571
1840 1845 1850	
acg ccg ttc acg ccg gat ggg cgc gca cac ggg gag ctg ccc gag caa Thr Pro Phe Thr Pro Asp Gly Arg Ala His Gly Glu Leu Pro Glu Gln	5619
1855 1860 1865	
cac aag cgt aag acg ctg ctc agc acc gac cac gcc ttc ccc tac atc His Lys Arg Lys Thr Leu Leu Ser Thr Asp His Ala Phe Pro Tyr Ile	5667
1870 1875 1880 1885	

aag Lys	act Thr	cgc Arg	atc Ile	cgt Arg	gtg Val	tgc Cys	cac His	cgg Arg	gag Glu	gag Glu	acg Thr	gtg Val	ctg Leu	acg Thr	cca Pro	5715
1890								1895				1900				
gtg Val	gag Glu	gtg Val	gcc Ala	atc Ile	gag Glu	gac Asp	atg Met	cag Gln	aag Lys	aag Lys	aca Thr	cgg Arg	gag Glu	ctg Leu	gcc Ala	5763
1905								1910				1915				
ttt Phe	gcc Ala	acc Thr	gag Glu	cag Gln	gac Asp	cca Pro	cca Pro	gat Asp	gct Ala	aag Lys	atg Met	cta Leu	cag Gln	atg Met	gtg Val	5811
1920								1925				1930				
ctt Leu	cag Gln	ggc Gly	tct Ser	gta Val	ggg Gly	ccc Pro	acc Thr	gtg Val	aac Asn	cag Gln	ggg Gly	ccc Pro	ctg Leu	gag Glu	gtg Val	5859
1935								1940				1945				
gcc Ala	cag Gln	gtg Val	ttt Phe	tta Leu	gca Ala	gag Glu	atc Ile	ccg Pro	gaa Glu	gac Asp	ccc Pro	aag Lys	ctc Leu	ttc Phe	cgg Arg	5907
1950				1955				1960				1965				
cat His	cac His	aac Asn	aaa Lys	ttg Leu	cgg Arg	ctc Leu	tgc Cys	ttc Phe	aag Lys	gac Asp	ttc Phe	tgc Cys	aag Lys	aaa Lys	tgt Cys	5955
1970								1975				1980				
gag Glu	gat Asp	gcg Ala	ctg Leu	cgg Arg	aaa Lys	aat Asn	aag Lys	gcc Ala	ctg Leu	att Ile	ggg Gly	ccg Pro	gac Asp	cag Gln	aag Lys	6003
1985								1990				1995				
gag Glu	tac Tyr	cac His	cgt Arg	gag Glu	ctg Leu	gag Glu	cgc Arg	aac Asn	tac Tyr	tgc Cys	cgc Arg	ctg Leu	cgg Arg	gag Glu	gct Ala	6051
2000								2005				2010				
ctg Leu	cag Gln	ccc Pro	ctg Leu	ctt Leu	acc Thr	cag Gln	cgc Arg	ctg Leu	ccc Pro	cag Gln	ctg Leu	atg Met	gca Ala	ccc Pro	acc Thr	6099
2015				2020				2025								
cca Pro	ccc Pro	ggc Gly	ctc Leu	agg Arg	aac Asn	tcc Ser	ttg Leu	aac Asn	aga Arg	gca Ala	agt Ser	ttc Phe	cga Arg	aag Lys	gca Ala	6147
2030				2035				2040				2045				
gac ctc tga gcccacaagg accaaagctg tacctagagg aaccagcacc Asp Leu																6196
cgggcctcag ctgtctgtgc tgcgagggga gtctgccctg gtgccactg ggctgtgggg																6256
tgaccacact gtacttgggg ctgggccctc tgcccctgtg tccccatctg tgtgcactga																6316
tgcttcctcc cttttttaat ttaaaatggt ttttataagc aaaaaaaaaa aaaaaa																6372

```
<210> 2
<211> 2047
<212> PRT
<213> Homo sapiens
```

<220>  
<223> full length human CLASP-7

```
<400> 2
Met Ala Ala Ser Glu Arg Arg Ala Phe Ala His Lys Ile Asn Arg Thr
   1                   5           10          15
```

Val Ala Ala Glu Val Arg Lys Gln Val Ser Arg Glu Arg Ser Gly Ser  
                     20                    25                    30  
 Pro His Ser Ser Arg Arg Cys Ser Ser Ser Leu Gly Val Pro Leu Thr  
                     35                    40                    45  
 Glu Val Val Glu Pro Leu Asp Phe Glu Asp Val Leu Leu Ser Arg Pro  
                     50                    55                    60  
 Pro Asp Ala Glu Pro Gly Pro Leu Arg Asp Leu Val Glu Phe Pro Ala  
                     65                    70                    75                    80  
 Asp Asp Leu Glu Leu Leu Leu Gln Pro Arg Glu Cys Arg Thr Thr Glu  
                     85                    90                    95  
 Pro Gly Ile Pro Lys Asp Glu Lys Leu Asp Ala Gln Val Arg Ala Ala  
                     100                    105                    110  
 Val Glu Met Tyr Ile Glu Asp Trp Val Ile Val His Arg Arg Tyr Gln  
                     115                    120                    125  
 Tyr Leu Ser Ala Ala Tyr Ser Pro Val Thr Thr Asp Thr Gln Arg Glu  
                     130                    135                    140  
 Arg Gln Lys Gly Leu Pro Arg Gln Val Phe Glu Gln Asp Ala Ser Gly  
                     145                    150                    155                    160  
 Asp Glu Arg Ser Gly Pro Glu Asp Ser Asn Asp Ser Arg Arg Gly Ser  
                     165                    170                    175  
 Gly Ser Pro Glu Asp Thr Pro Arg Ser Ser Gly Ala Ser Ser Ile Phe  
                     180                    185                    190  
 Asp Leu Arg Asn Leu Ala Ala Asp Ser Leu Leu Pro Ser Leu Leu Glu  
                     195                    200                    205  
 Arg Ala Ala Pro Glu Asp Val Asp Arg Arg Asn Glu Thr Leu Arg Arg  
                     210                    215                    220  
 Gln His Arg Pro Pro Ala Leu Leu Thr Leu Tyr Pro Ala Pro Asp Glu  
                     225                    230                    235                    240  
 Asp Glu Ala Val Glu Arg Cys Ser Arg Pro Glu Pro Pro Arg Glu His  
                     245                    250                    255  
 Phe Gly Gln Arg Ile Leu Val Lys Cys Leu Ser Leu Lys Phe Glu Ile  
                     260                    265                    270  
 Glu Ile Glu Pro Ile Phe Gly Ile Leu Ala Leu Tyr Asp Val Arg Glu  
                     275                    280                    285  
 Lys Lys Lys Ile Ser Glu Asn Phe Tyr Phe Asp Leu Asn Ser Asp Ser  
                     290                    295                    300  
 Met Lys Gly Leu Leu Arg Ala His Gly Thr His Pro Ala Ile Ser Thr  
                     305                    310                    315                    320  
 Leu Ala Arg Ser Ala Ile Phe Ser Val Thr Tyr Pro Ser Pro Asp Ile  
                     325                    330                    335

Phe Leu Val Ile Lys Leu Glu Lys Val Leu Gln Gln Gly Asp Ile Ser  
 340 345 350  
 Glu Cys Cys Glu Pro Tyr Met Val Leu Lys Glu Val Asp Thr Ala Lys  
 355 360 365  
 Asn Lys Glu Lys Leu Glu Lys Leu Arg Leu Ala Ala Glu Gln Phe Cys  
 370 375 380  
 Thr Arg Leu Gly Arg Tyr Arg Met Pro Phe Ala Trp Thr Ala Val His  
 385 390 395 400  
 Leu Ala Asn Ile Val Ser Ser Ala Gly Gln Leu Asp Arg Asp Ser Asp  
 405 410 415  
 Ser Glu Gly Glu Arg Arg Pro Ala Trp Thr Asp Arg Arg Arg Arg Gly  
 420 425 430  
 Pro Gln Asp Arg Ala Ser Ser Gly Asp Asp Ala Cys Ser Phe Ser Gly  
 435 440 445  
 Phe Arg Pro Ala Thr Leu Thr Val Thr Asn Phe Phe Lys Gln Glu Ala  
 450 455 460  
 Glu Arg Leu Ser Asp Glu Asp Leu Phe Lys Phe Leu Ala Asp Met Arg  
 465 470 475 480  
 Arg Pro Ser Ser Leu Leu Arg Arg Leu Arg Pro Val Thr Ala Gln Leu  
 485 490 495  
 Lys Ile Asp Ile Ser Pro Ala Pro Glu Asn Pro His Phe Cys Leu Ser  
 500 505 510  
 Pro Glu Leu Leu His Ile Lys Pro Tyr Pro Asp Pro Arg Gly Arg Pro  
 515 520 525  
 Thr Lys Glu Ile Leu Glu Phe Pro Ala Arg Glu Val Tyr Ala Pro His  
 530 535 540  
 Thr Ser Tyr Arg Asn Leu Leu Tyr Val Tyr Pro His Ser Leu Asn Phe  
 545 550 555 560  
 Ser Ser Arg Gln Gly Ser Val Arg Asn Leu Ala Val Arg Val Gln Tyr  
 565 570 575  
 Met Thr Gly Glu Asp Pro Ser Gln Ala Leu Pro Val Ile Phe Gly Lys  
 580 585 590  
 Ser Ser Cys Ser Glu Phe Thr Arg Glu Ala Phe Thr Pro Val Val Tyr  
 595 600 605  
 His Asn Lys Ser Pro Glu Phe Tyr Glu Glu Phe Lys Leu His Leu Pro  
 610 615 620  
 Ala Cys Val Thr Glu Asn His His Leu Leu Phe Thr Phe Tyr His Val  
 625 630 635 640  
 Ser Cys Gln Pro Arg Pro Gly Thr Ala Leu Glu Thr Pro Val Gly Phe  
 645 650 655  
 Thr Trp Ile Pro Leu Leu Gln His Gly Arg Leu Arg Thr Gly Pro Phe

660						665						670					
Cys	Leu	Pro	Val	Ser	Val	Asp	Gln	Pro	Pro	Pro	Ser	Tyr	Ser	Val	Leu		
		675					680					685					
Thr	Pro	Asp	Val	Ala	Leu	Pro	Gly	Met	Arg	Trp	Val	Asp	Gly	His	Lys		
	690					695					700						
Gly	Val	Phe	Ser	Val	Glu	Leu	Thr	Ala	Val	Ser	Ser	Val	His	Pro	Gln		
705					710					715					720		
Asp	Pro	Tyr	Leu	Asp	Lys	Phe	Phe	Thr	Leu	Val	His	Val	Leu	Glu	Glu		
				725					730					735			
Gly	Ala	Phe	Pro	Phe	Arg	Leu	Lys	Asp	Thr	Val	Leu	Ser	Glu	Gly	Asn		
			740					745					750				
Val	Glu	Gln	Glu	Leu	Arg	Ala	Ser	Leu	Ala	Ala	Leu	Arg	Leu	Ala	Ser		
		755					760					765					
Pro	Glu	Pro	Leu	Val	Ala	Phe	Ser	His	His	Val	Leu	Asp	Lys	Leu	Val		
	770					775					780						
Arg	Leu	Val	Ile	Arg	Pro	Pro	Ile	Ile	Ser	Gly	Gln	Ile	Val	Asn	Leu		
785					790					795					800		
Gly	Arg	Gly	Ala	Phe	Glu	Ala	Met	Ala	His	Val	Val	Ser	Leu	Val	His		
				805					810					815			
Arg	Ser	Leu	Glu	Ala	Ala	Gln	Asp	Ala	Arg	Gly	His	Cys	Pro	Gln	Leu		
			820					825					830				
Ala	Ala	Tyr	Val	His	Tyr	Ala	Phe	Arg	Leu	Pro	Gly	Thr	Glu	Pro	Ser		
		835					840					845					
Leu	Pro	Asp	Gly	Ala	Pro	Pro	Val	Thr	Val	Gln	Ala	Ala	Thr	Leu	Ala		
	850					855					860						
Arg	Gly	Ser	Gly	Arg	Pro	Ala	Ser	Leu	Tyr	Leu	Ala	Arg	Ser	Lys	Ser		
865					870					875					880		
Ile	Ser	Ser	Ser	Asn	Pro	Asp	Leu	Ala	Val	Ala	Pro	Gly	Ser	Val	Asp		
				885					890					895			
Asp	Glu	Val	Ser	Arg	Ile	Leu	Ala	Ser	Lys	Leu	Leu	His	Glu	Glu	Leu		
			900					905					910				
Ala	Leu	Gln	Trp	Val	Val	Ser	Ser	Ser	Ala	Val	Arg	Glu	Ala	Ile	Leu		
		915					920					925					
Gln	His	Ala	Trp	Phe	Phe	Phe	Gln	Leu	Met	Val	Lys	Ser	Met	Ala	Leu		
	930					935					940						
His	Leu	Leu	Leu	Gly	Gln	Arg	Leu	Asp	Thr	Pro	Arg	Lys	Leu	Arg	Phe		
945					950					955					960		
Pro	Gly	Arg	Phe	Leu	Asp	Asp	Ile	Thr	Ala	Leu	Val	Gly	Ser	Val	Gly		
				965					970					975			
Leu	Glu	Val	Ile	Thr	Arg	Val	His	Lys	Asp	Val	Glu	Leu	Ala	Glu	His		
			980					985					990				

Leu Asn Ala Ser Leu Ala Phe Phe Leu Ser Asp Leu Leu Ser Leu Val  
 995 1000 1005  
 Asp Arg Gly Phe Val Phe Ser Leu Val Arg Ala His Tyr Lys Gln Val  
 1010 1015 1020  
 Ala Thr Arg Leu Gln Ser Ser Pro Asn Pro Ala Ala Leu Leu Thr Leu  
 1025 1030 1035 1040  
 Arg Met Glu Phe Thr Arg Ile Leu Cys Ser His Glu His Tyr Val Thr  
 1045 1050 1055  
 Leu Asn Leu Pro Cys Cys Pro Leu Ser Pro Pro Ala Ser Pro Ser Pro  
 1060 1065 1070  
 Ser Val Ser Ser Thr Thr Ser Gln Ser Ser Thr Phe Ser Ser Gln Ala  
 1075 1080 1085  
 Pro Asp Pro Lys Val Thr Ser Met Phe Glu Leu Ser Gly Pro Phe Arg  
 1090 1095 1100  
 Gln Gln His Phe Leu Ala Gly Leu Leu Leu Thr Glu Leu Ala Leu Ala  
 1105 1110 1115 1120  
 Leu Glu Pro Glu Ala Glu Gly Ala Phe Leu Leu His Lys Lys Ala Ile  
 1125 1130 1135  
 Ser Ala Val His Ser Leu Leu Cys Gly His Asp Thr Asp Pro Arg Tyr  
 1140 1145 1150  
 Ala Glu Ala Thr Val Lys Ala Arg Val Ala Glu Leu Tyr Leu Pro Leu  
 1155 1160 1165  
 Leu Ser Ile Ala Arg Asp Thr Leu Pro Arg Leu His Asp Phe Ala Glu  
 1170 1175 1180  
 Gly Pro Gly Gln Arg Ser Arg Leu Ala Ser Met Leu Asp Ser Asp Thr  
 1185 1190 1195 1200  
 Glu Gly Glu Gly Asp Ile Ala Gly Thr Ile Asn Pro Ser Val Ala Met  
 1205 1210 1215  
 Ala Ile Ala Gly Gly Pro Leu Ala Pro Gly Ser Arg Ala Ser Ile Ser  
 1220 1225 1230  
 Gln Gly Pro Pro Thr Ala Ser Arg Ala Gly Cys Ala Leu Ser Ala Glu  
 1235 1240 1245  
 Ser Ser Arg Thr Leu Leu Ala Cys Val Leu Trp Val Leu Lys Asn Thr  
 1250 1255 1260  
 Glu Pro Ala Leu Leu Gln Arg Trp Ala Thr Asp Leu Thr Leu Pro Gln  
 1265 1270 1275 1280  
 Leu Gly Arg Leu Leu Asp Leu Leu Tyr Leu Cys Leu Ala Ala Phe Glu  
 1285 1290 1295  
 Tyr Lys Gly Lys Lys Ala Phe Glu Arg Ile Asn Ser Leu Thr Phe Lys  
 1300 1305 1310

Lys Ser Leu Asp Met Lys Ala Arg Leu Glu Glu Ala Ile Leu Gly Thr  
 1315 1320 1325  
 Ile Gly Ala Arg Gln Glu Met Val Arg Arg Ser Arg Glu Arg Ser Pro  
 1330 1335 1340  
 Phe Gly Asn Pro Glu Asn Val Arg Trp Arg Lys Ser Val Thr His Trp  
 1345 1350 1355 1360  
 Lys Gln Thr Ser Asp Arg Val Asp Lys Thr Lys Asp Glu Met Glu His  
 1365 1370 1375  
 Glu Ala Leu Val Glu Gly Asn Leu Ala Thr Glu Ala Ser Leu Val Val  
 1380 1385 1390  
 Leu Asp Thr Leu Glu Ile Ile Val Gln Thr Val Met Leu Ser Glu Ala  
 1395 1400 1405  
 Arg Glu Ser Val Leu Gly Ala Val Leu Lys Val Val Leu Tyr Ser Leu  
 1410 1415 1420  
 Gly Ser Ala Gln Ser Ala Leu Phe Leu Gln His Gly Leu Ala Thr Gln  
 1425 1430 1435 1440  
 Arg Ala Leu Val Ser Lys Phe Pro Glu Leu Leu Phe Glu Glu Asp Thr  
 1445 1450 1455  
 Glu Leu Cys Ala Asp Leu Cys Leu Arg Leu Leu Arg His Cys Gly Ser  
 1460 1465 1470  
 Arg Ile Ser Thr Ile Arg Thr His Ala Ser Ala Ser Leu Tyr Leu Leu  
 1475 1480 1485  
 Met Arg Gln Asn Phe Glu Ile Gly His Asn Phe Ala Arg Val Lys Met  
 1490 1495 1500  
 Gln Val Thr Met Ser Leu Ser Ser Leu Val Gly Thr Thr Gln Asn Phe  
 1505 1510 1515 1520  
 Ser Glu Glu His Leu Arg Arg Ser Leu Lys Thr Ile Leu Thr Tyr Ala  
 1525 1530 1535  
 Glu Glu Asp Met Gly Leu Arg Asp Ser Thr Phe Ala Glu Gln Val Gln  
 1540 1545 1550  
 Asp Leu Met Phe Asn Leu His Met Ile Leu Thr Asp Thr Val Lys Met  
 1555 1560 1565  
 Lys Glu His Gln Glu Asp Pro Glu Met Leu Ile Asp Leu Met Tyr Arg  
 1570 1575 1580  
 Ile Ala Arg Gly Tyr Gln Gly Ser Pro Asp Leu Arg Leu Thr Trp Leu  
 1585 1590 1595 1600  
 Gln Asn Met Ala Gly Lys His Ala Glu Leu Gly Asn His Ala Glu Ala  
 1605 1610 1615  
 Ala Gln Cys Met Val His Ala Ala Ala Leu Val Ala Glu Tyr Leu Ala  
 1620 1625 1630  
 Leu Leu Glu Asp Gln Arg His Leu Pro Val Gly Cys Val Ser Phe Gln

1635	1640	1645
Asn Ile Ser Ser Asn Val Leu Glu Glu Ser Ala Ile Ser Asp Asp Ile 1650 1655 1660		
Leu Ser Pro Asp Glu Glu Gly Phe Cys Ser Gly Lys His Phe Thr Glu 1665 1670 1675 1680		
Leu Gly Leu Val Gly Leu Leu Glu Gln Ala Ala Gly Tyr Phe Thr Met 1685 1690 1695		
Gly Gly Leu Tyr Glu Ala Val Asn Glu Val Tyr Lys Asn Leu Ile Pro 1700 1705 1710		
Ile Leu Glu Ala His Arg Asp Tyr Lys Lys Leu Ala Ala Val His Gly 1715 1720 1725		
Lys Leu Gln Glu Ala Phe Thr Lys Ile Met His Gln Ser Ser Gly Trp 1730 1735 1740		
Glu Arg Val Phe Gly Thr Tyr Phe Arg Val Gly Phe Tyr Gly Ala His 1745 1750 1755 1760		
Phe Gly Asp Leu Asp Glu Gln Glu Phe Val Tyr Lys Glu Pro Ser Ile 1765 1770 1775		
Thr Lys Leu Ala Glu Ile Ser His Arg Leu Glu Glu Phe Tyr Thr Glu 1780 1785 1790		
Arg Phe Gly Asp Asp Val Val Glu Ile Ile Lys Asp Ser Tyr Pro Val 1795 1800 1805		
Asp Lys Ser Lys Leu Asp Ser Gln Lys Ala Tyr Ile Gln Ile Thr Tyr 1810 1815 1820		
Val Glu Pro Tyr Phe Asp Thr Tyr Glu Leu Lys Asp Arg Val Thr Tyr 1825 1830 1835 1840		
Phe Asp Arg Asn Tyr Gly Leu Arg Thr Phe Leu Phe Cys Thr Pro Phe 1845 1850 1855		
Thr Pro Asp Gly Arg Ala His Gly Glu Leu Pro Glu Gln His Lys Arg 1860 1865 1870		
Lys Thr Leu Leu Ser Thr Asp His Ala Phe Pro Tyr Ile Lys Thr Arg 1875 1880 1885		
Ile Arg Val Cys His Arg Glu Glu Thr Val Leu Thr Pro Val Glu Val 1890 1895 1900		
Ala Ile Glu Asp Met Gln Lys Lys Thr Arg Glu Leu Ala Phe Ala Thr 1905 1910 1915 1920		
Glu Gln Asp Pro Pro Asp Ala Lys Met Leu Gln Met Val Leu Gln Gly 1925 1930 1935		
Ser Val Gly Pro Thr Val Asn Gln Gly Pro Leu Glu Val Ala Gln Val 1940 1945 1950		
Phe Leu Ala Glu Ile Pro Glu Asp Pro Lys Leu Phe Arg His His Asn 1955 1960 1965		



Lys Leu Arg Leu Cys Phe Lys Asp Phe Cys Lys Lys Cys Glu Asp Ala  
 1970 1975 1980

Leu Arg Lys Asn Lys Ala Leu Ile Gly Pro Asp Gln Lys Glu Tyr His  
 1985 1990 1995 2000

Arg Glu Leu Glu Arg Asn Tyr Cys Arg Leu Arg Glu Ala Leu Gln Pro  
 2005 2010 2015

Leu Leu Thr Gln Arg Leu Pro Gln Leu Met Ala Pro Thr Pro Pro Gly  
 2020 2025 2030

Leu Arg Asn Ser Leu Asn Arg Ala Ser Phe Arg Lys Ala Asp Leu  
 2035 2040 2045

<210> 3

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: furin protease  
 consensus cleavage sequence

<400> 3

Arg Lys Gln Arg  
 1

<210> 4

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CLASP-7 homolog  
 of furin protease consensus cleavage sequence

<400> 4

Arg Lys Leu Arg  
 1

<210> 5

<211> 10

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence: CLASP-7  
 immunoreceptor tyrosine-based activation motif  
 (ITAM) 1

<220>

<221> MOD\_RES

<222> (1)..(10)

<223> Xaa = any amino acid

<400> 5

Tyr Xaa Xaa Val Xaa Xaa Tyr Xaa Xaa His  
 1 5 10

<210> 6  
 <211> 13  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:CLASP-7  
 immunoreceptor tyrosine-based activation motif  
 (ITAM) 2

<220>  
 <221> MOD\_RES  
 <222> (1)..(13)  
 <223> Xaa = any amino acid

<400> 6  
 Tyr Xaa Xaa Ile Xaa Xaa Xaa Xaa Xaa Tyr Xaa Xaa Thr  
 1 5 10

<210> 7  
 <211> 9  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:highly  
 conserved non-tyrosine containing region from  
 motif E

<220>  
 <221> MOD\_RES  
 <222> (2)  
 <223> Xaa = conservative amino acid substitution, Ile or Leu

<220>  
 <221> MOD\_RES  
 <222> (4)  
 <223> Xaa = any amino acid

<220>  
 <221> MOD\_RES  
 <222> (7)  
 <223> Xaa = conservative amino acid substitution, Asp,  
 Glu or Gln

<220>  
 <221> MOD\_RES  
 <222> (8)  
 <223> Xaa = any amino acid

<400> 7  
 Pro Xaa Glu Xaa Ala Ile Xaa Xaa Met  
 1 5

<210> 8

<211> 16  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:highly  
 conserved non-tyrosine containing region from  
 motif F

<220>  
 <221> MOD\_RES  
 <222> (2)..(4)  
 <223> Xaa = any amino acid

<220>  
 <221> MOD\_RES  
 <222> (6)  
 <223> Xaa = conservative amino acid substitution, Gln or Asn

<220>  
 <221> MOD\_RES  
 <222> (8)..(15)  
 <223> Xaa = any amino acid

<400> 8  
 Leu Xaa Met Xaa Leu Xaa Gly Xaa Val Xaa Xaa Xaa Val Asn Xaa Gly  
           1                  5                  10                  15

<210> 9  
 <211> 1352  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> human CLASP-2A

<400> 9  
 Val Leu His His His Gln Asn Pro Glu Phe Tyr Asp Glu Ile Lys Ile  
           1                  5                  10                  15  
 Glu Leu Pro Thr Gln Leu His Glu Lys His His Leu Leu Leu Thr Phe  
                   20                  25                  30  
 Phe His Val Ser Cys Asp Asn Ser Ser Lys Gly Ser Thr Lys Lys Arg  
           35                  40                  45  
 Asp Val Val Glu Thr Gln Val Gly Tyr Ser Trp Leu Pro Leu Leu Lys  
           50                  55                  60  
 Asp Gly Arg Val Val Thr Ser Glu Gln His Ile Pro Val Ser Ala Asn  
           65                  70                  75                  80  
 Leu Pro Ser Gly Tyr Leu Gly Tyr Gln Glu Leu Gly Met Gly Arg His  
                   85                  90                  95  
 Tyr Gly Pro Glu Ile Lys Trp Val Asp Gly Gly Lys Pro Leu Leu Lys  
           100                  105                  110  
 Ile Ser Thr His Leu Val Ser Thr Val Tyr Thr Gln Asp Gln His Leu  
           115                  120                  125

His Asn Phe Phe Gln Tyr Cys Gln Lys Thr Glu Ser Gly Ala Gln Ala  
 130 135 140  
 Leu Gly Asn Glu Leu Val Lys Tyr Leu Lys Ser Leu His Ala Met Glu  
 145 150 155 160  
 Gly His Val Met Ile Ala Phe Leu Pro Thr Ile Leu Asn Gln Leu Phe  
 165 170 175  
 Arg Val Leu Thr Arg Ala Thr Gln Glu Glu Val Ala Val Asn Val Thr  
 180 185 190  
 Arg Val Ile Ile His Val Val Ala Gln Cys His Glu Glu Gly Leu Glu  
 195 200 205  
 Ser His Leu Arg Ser Tyr Val Lys Tyr Ala Tyr Lys Ala Glu Pro Tyr  
 210 215 220  
 Val Ala Ser Glu Tyr Lys Thr Val His Glu Glu Leu Thr Lys Ser Met  
 225 230 235 240  
 Thr Thr Ile Leu Lys Pro Ser Ala Asp Phe Leu Thr Ser Asn Lys Leu  
 245 250 255  
 Leu Arg Tyr Ser Trp Phe Phe Phe Asp Val Leu Ile Lys Ser Met Ala  
 260 265 270  
 Gln His Leu Ile Glu Asn Ser Lys Val Lys Leu Leu Arg Asn Gln Arg  
 275 280 285  
 Phe Pro Ala Ser Tyr His His Ala Ala Glu Thr Val Val Asn Met Leu  
 290 295 300  
 Met Pro His Ile Thr Gln Lys Phe Gly Asp Asn Pro Glu Ala Ser Lys  
 305 310 315 320  
 Asn Ala Asn His Ser Leu Ala Val Phe Ile Lys Arg Cys Phe Thr Phe  
 325 330 335  
 Met Asp Arg Gly Phe Val Phe Lys Gln Ile Asn Asn Tyr Ile Ser Cys  
 340 345 350  
 Phe Ala Pro Gly Asp Pro Lys Thr Leu Phe Glu Tyr Lys Phe Glu Phe  
 355 360 365  
 Leu Arg Val Val Cys Asn His Glu His Tyr Ile Pro Leu Asn Leu Pro  
 370 375 380  
 Met Pro Phe Gly Lys Gly Arg Ile Gln Arg Tyr Gln Asp Leu Gln Leu  
 385 390 395 400  
 Asp Tyr Ser Leu Thr Asp Glu Phe Cys Arg Asn His Phe Leu Val Gly  
 405 410 415  
 Leu Leu Leu Arg Glu Val Gly Thr Ala Leu Gln Glu Phe Arg Glu Val  
 420 425 430  
 Arg Leu Ile Ala Ile Ser Val Leu Lys Asn Leu Leu Ile Lys His Ser  
 435 440 445

Phe Asp Asp Arg Tyr Ala Ser Arg Ser His Gln Ala Arg Ile Ala Thr  
 450 455 460  
 Leu Tyr Leu Pro Leu Phe Gly Leu Leu Ile Glu Asn Val Gln Arg Ile  
 465 470 475 480  
 Asn Val Arg Asp Val Ser Pro Phe Pro Val Asn Ala Gly Met Thr Val  
 485 490 495  
 Lys Asp Glu Ser Leu Ala Leu Pro Ala Val Asn Pro Leu Val Thr Pro  
 500 505 510  
 Gln Lys Gly Ser Thr Leu Asp Asn Ser Leu His Lys Asp Leu Leu Gly  
 515 520 525  
 Ala Ile Ser Gly Ile Ala Ser Pro Tyr Thr Thr Ser Thr Pro Asn Ile  
 530 535 540  
 Asn Ser Val Arg Asn Ala Asp Ser Arg Gly Ser Leu Ile Ser Thr Asp  
 545 550 555 560  
 Ser Gly Asn Ser Leu Pro Glu Arg Asn Ser Glu Lys Ser Asn Ser Leu  
 565 570 575  
 Asp Lys His Gln Gln Ser Ser Thr Leu Gly Asn Ser Val Val Arg Cys  
 580 585 590  
 Asp Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu Leu Met Cys Phe Leu  
 595 600 605  
 Tyr Ile Leu Lys Ser Met Ser Asp Asp Ala Leu Phe Thr Tyr Trp Asn  
 610 615 620  
 Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe Thr Ile Ser Glu Val  
 625 630 635 640  
 Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg Tyr Ile Ala Arg Asn  
 645 650 655  
 Gln Glu Gly Leu Gly Pro Ile Val His Asp Arg Lys Ser Gln Thr Leu  
 660 665 670  
 Pro Val Ser Arg Asn Arg Thr Gly Met Met His Ala Arg Leu Gln Gln  
 675 680 685  
 Leu Gly Ser Leu Asp Asn Ser Leu Thr Phe Asn His Ser Tyr Gly His  
 690 695 700  
 Ser Asp Ala Asp Val Leu His Gln Ser Leu Leu Glu Ala Asn Ile Ala  
 705 710 715 720  
 Thr Glu Val Cys Leu Thr Ala Leu Asp Thr Leu Ser Leu Phe Thr Leu  
 725 730 735  
 Ala Phe Lys Asn Gln Leu Leu Ala Asp His Gly His Asn Pro Leu Met  
 740 745 750  
 Lys Lys Val Phe Asp Val Tyr Leu Cys Phe Leu Gln Lys His Gln Ser  
 755 760 765  
 Glu Thr Ala Leu Lys Asn Val Phe Thr Ala Leu Arg Ser Leu Ile Tyr

770					775					780					
Lys	Phe	Pro	Ser	Thr	Phe	Tyr	Glu	Gly	Arg	Ala	Asp	Met	Cys	Ala	Ala
785					790					795					800
Leu	Cys	Tyr	Glu	Ile	Leu	Lys	Cys	Cys	Asn	Ser	Lys	Leu	Ser	Ser	Ile
				805					810					815	
Arg	Thr	Glu	Ala	Ser	Gln	Leu	Leu	Tyr	Phe	Leu	Met	Arg	Asn	Asn	Phe
			820					825					830		
Asp	Tyr	Thr	Gly	Lys	Lys	Ser	Phe	Val	Arg	Thr	His	Leu	Gln	Val	Ile
			835				840					845			
Ile	Ser	Val	Ser	Gln	Leu	Ile	Ala	Asp	Val	Val	Gly	Ile	Gly	Glu	Thr
	850					855					860				
Arg	Phe	Gln	Gln	Ser	Leu	Ser	Ile	Ile	Asn	Asn	Cys	Ala	Asn	Ser	Asp
865					870					875					880
Arg	Leu	Ile	Lys	His	Thr	Ser	Phe	Ser	Ser	Asp	Val	Lys	Asp	Leu	Thr
				885					890					895	
Lys	Arg	Ile	Arg	Thr	Val	Leu	Met	Ala	Thr	Ala	Gln	Met	Lys	Glu	His
			900					905					910		
Glu	Asn	Asp	Pro	Glu	Met	Leu	Val	Asp	Leu	Gln	Tyr	Ser	Leu	Ala	Lys
		915					920					925			
Ser	Tyr	Ala	Ser	Thr	Pro	Glu	Leu	Arg	Lys	Thr	Trp	Leu	Asp	Ser	Met
	930					935					940				
Ala	Arg	Ile	His	Val	Lys	Asn	Gly	Asp	Leu	Ser	Glu	Ala	Ala	Met	Cys
945					950					955					960
Tyr	Val	His	Val	Thr	Ala	Leu	Val	Ala	Glu	Tyr	Leu	Thr	Arg	Lys	Gly
				965					970					975	
Val	Phe	Arg	Gln	Gly	Cys	Thr	Ala	Phe	Arg	Val	Ile	Thr	Pro	Asn	Ile
			980					985					990		
Asp	Glu	Glu	Ala	Ser	Met	Met	Glu	Asp	Val	Gly	Met	Gln	Asp	Val	His
		995					1000					1005			
Phe	Asn	Glu	Asp	Val	Leu	Met	Glu	Leu	Leu	Glu	Gln	Cys	Ala	Asp	Gly
	1010					1015					1020				
Leu	Trp	Lys	Ala	Glu	Arg	Tyr	Glu	Leu	Ile	Ala	Asp	Ile	Tyr	Lys	Leu
1025					1030					1035					1040
Ile	Ile	Pro	Ile	Tyr	Glu	Lys	Arg	Arg	Asp	Phe	Phe	Glu	Asp	Glu	Asp
			1045						1050				1055		
Gly	Lys	Glu	Tyr	Ile	Tyr	Lys	Glu	Pro	Lys	Leu	Thr	Pro	Leu	Ser	Glu
		1060					1065					1070			
Ile	Ser	Gln	Arg	Leu	Leu	Lys	Leu	Tyr	Ser	Asp	Lys	Phe	Gly	Ser	Glu
	1075					1080					1085				
Asn	Val	Lys	Met	Ile	Gln	Asp	Ser	Gly	Lys	Val	Asn	Pro	Lys	Asp	Leu
	1090					1095					1100				

Asp Ser Lys Tyr Ala Tyr Ile Gln Val Thr His Val Ile Pro Phe Phe  
 1105 1110 1115 1120  
 Asp Glu Lys Glu Leu Gln Glu Arg Lys Thr Glu Phe Glu Arg Ser His  
 1125 1130 1135  
 Asn Ile Arg Arg Phe Met Phe Glu Met Pro Phe Thr Gln Thr Gly Lys  
 1140 1145 1150  
 Arg Gln Gly Gly Val Glu Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr  
 1155 1160 1165  
 Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg Ile Pro Val Met Tyr  
 1170 1175 1180  
 Gln His His Thr Asp Leu Asn Pro Ile Glu Val Ala Ile Asp Glu Met  
 1185 1190 1195 1200  
 Ser Lys Lys Val Ala Glu Leu Arg Gln Leu Cys Ser Ser Ala Glu Val  
 1205 1210 1215  
 Asp Met Ile Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln  
 1220 1225 1230  
 Val Asn Ala Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr  
 1235 1240 1245  
 Asn Thr Lys Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val  
 1250 1255 1260  
 Phe Arg Gln Phe Val Glu Ala Cys Gly Gln Ala Leu Ala Val Asn Glu  
 1265 1270 1275 1280  
 Arg Leu Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu Glu Met Lys Ala  
 1285 1290 1295  
 Asn Tyr Arg Glu Met Ala Lys Glu Leu Ser Glu Ile Met His Glu Gln  
 1300 1305 1310  
 Ile Cys Pro Leu Glu Glu Lys Thr Ser Val Leu Pro Asn Ser Leu His  
 1315 1320 1325  
 Ile Phe Asn Ala Ile Ser Gly Thr Pro Thr Ser Thr Met Val His Gly  
 1330 1335 1340  
 Met Thr Ser Ser Ser Ser Val Val  
 1345 1350

<210> 10  
 <211> 1534  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> human KIAA1058

<400> 10  
 Ala Ser Gly Asn Leu Asp Lys Asn Ala Arg Phe Ser Ala Ile Tyr Arg  
 1 5 10 15

Gln Asp Ser Asn Lys Leu Ser Asn Asp Asp Met Leu Lys Leu Leu Ala  
                   20                                  25                                  30  
 Asp Phe Arg Lys Pro Glu Lys Met Ala Lys Leu Pro Val Ile Leu Gly  
                   35                                  40                                  45  
 Asn Leu Asp Ile Thr Ile Asp Asn Val Ser Ser Asp Phe Pro Asn Tyr  
           50                                  55                                  60  
 Val Asn Ser Ser Tyr Ile Pro Thr Lys Gln Phe Glu Thr Cys Ser Lys  
   65                                  70                                  75                                  80  
 Thr Pro Ile Thr Phe Glu Val Glu Glu Phe Val Pro Cys Ile Pro Lys  
                                   85                                  90                                  95  
 His Thr Gln Pro Tyr Thr Ile Tyr Thr Asn His Leu Tyr Val Tyr Pro  
                   100                                  105                                  110  
 Lys Tyr Leu Lys Tyr Asp Ser Gln Lys Ser Phe Ala Lys Ala Arg Asn  
           115                                  120                                  125  
 Ile Ala Ile Cys Ile Glu Phe Lys Asp Ser Asp Glu Glu Asp Ser Gln  
   130                                  135                                  140  
 Pro Leu Lys Cys Ile Tyr Gly Arg Pro Gly Gly Pro Val Phe Thr Arg  
 145                                  150                                  155                                  160  
 Ser Ala Phe Ala Ala Val Leu His His His Gln Asn Pro Glu Phe Tyr  
                                   165                                  170                                  175  
 Asp Glu Ile Lys Ile Glu Leu Pro Thr Gln Leu His Glu Lys His His  
                   180                                  185                                  190  
 Leu Leu Leu Thr Phe Phe His Val Ser Cys Asp Asn Ser Ser Lys Gly  
   195                                  200                                  205  
 Ser Thr Lys Lys Arg Asp Val Val Glu Thr Gln Val Gly Tyr Ser Trp  
   210                                  215                                  220  
 Leu Pro Leu Leu Lys Asp Gly Arg Val Val Thr Ser Glu Gln His Ile  
 225                                  230                                  235                                  240  
 Pro Val Ser Ala Asn Leu Pro Ser Gly Tyr Leu Gly Tyr Gln Glu Leu  
                                   245                                  250                                  255  
 Gly Met Gly Arg His Tyr Gly Pro Glu Ile Lys Trp Val Asp Gly Gly  
                   260                                  265                                  270  
 Lys Pro Leu Leu Lys Ile Ser Thr His Leu Val Ser Thr Val Tyr Thr  
           275                                  280                                  285  
 Gln Asp Gln His Leu His Asn Phe Phe Gln Tyr Cys Gln Lys Thr Glu  
   290                                  295                                  300  
 Ser Gly Ala Gln Ala Leu Gly Asn Glu Leu Val Lys Tyr Leu Lys Ser  
 305                                  310                                  315                                  320  
 Leu His Ala Met Glu Gly His Val Met Ile Ala Phe Leu Pro Thr Ile  
                                   325                                  330                                  335



Leu Asn Gln Leu Phe Arg Val Leu Thr Arg Ala Thr Gln Glu Glu Val  
 340 345 350  
 Ala Val Asn Val Thr Arg Val Ile Ile His Val Val Ala Gln Cys His  
 355 360 365  
 Glu Glu Gly Leu Glu Ser His Leu Arg Ser Tyr Val Lys Tyr Ala Tyr  
 370 375 380  
 Lys Ala Glu Pro Tyr Val Ala Ser Glu Tyr Lys Thr Val His Glu Glu  
 385 390 395 400  
 Leu Thr Lys Ser Met Thr Thr Ile Leu Lys Pro Ser Ala Asp Phe Leu  
 405 410 415  
 Thr Ser Asn Lys Leu Leu Lys Tyr Ser Trp Phe Phe Phe Asp Val Leu  
 420 425 430  
 Ile Lys Ser Met Ala Gln His Leu Ile Glu Asn Ser Lys Val Lys Leu  
 435 440 445  
 Leu Arg Asn Gln Arg Phe Pro Ala Ser Tyr His His Ala Val Glu Thr  
 450 455 460  
 Val Val Asn Met Leu Met Pro His Ile Thr Gln Lys Phe Arg Asp Asn  
 465 470 475 480  
 Pro Glu Ala Ser Lys Asn Ala Asn His Ser Leu Ala Val Phe Ile Lys  
 485 490 495  
 Arg Cys Phe Thr Phe Met Asp Arg Gly Phe Val Phe Lys Gln Ile Asn  
 500 505 510  
 Asn Tyr Ile Ser Cys Phe Ala Pro Gly Asp Pro Lys Thr Leu Phe Glu  
 515 520 525  
 Tyr Lys Phe Glu Phe Leu Arg Val Val Cys Asn His Glu His Tyr Ile  
 530 535 540  
 Pro Leu Asn Leu Pro Met Pro Phe Gly Lys Gly Arg Ile Gln Arg Tyr  
 545 550 555 560  
 Gln Asp Leu Gln Leu Asp Tyr Ser Leu Thr Asp Glu Phe Cys Arg Asn  
 565 570 575  
 His Phe Leu Val Gly Leu Leu Leu Arg Glu Val Gly Thr Ala Leu Gln  
 580 585 590  
 Glu Phe Arg Glu Val Arg Leu Ile Ala Ile Ser Val Leu Lys Asn Leu  
 595 600 605  
 Leu Ile Lys His Ser Phe Asp Asp Arg Tyr Ala Ser Arg Ser His Gln  
 610 615 620  
 Ala Arg Ile Ala Thr Leu Tyr Leu Pro Leu Phe Gly Leu Leu Ile Glu  
 625 630 635 640  
 Asn Val Gln Arg Ile Asn Val Arg Asp Val Ser Pro Phe Pro Val Asn  
 645 650 655  
 Ala Gly Met Thr Val Lys Asp Glu Ser Leu Ala Leu Pro Ala Val Asn

660					665					670					
Pro	Leu	Val	Thr	Pro	Gln	Lys	Gly	Ser	Thr	Leu	Asp	Asn	Ser	Leu	His
	675						680					685			
Lys	Asp	Leu	Leu	Gly	Ala	Ile	Ser	Gly	Ile	Ala	Ser	Pro	Tyr	Thr	Thr
	690					695					700				
Ser	Thr	Pro	Asn	Ile	Asn	Ser	Val	Arg	Asn	Ala	Asp	Ser	Arg	Gly	Ser
705					710					715					720
Leu	Ile	Ser	Thr	Asp	Ser	Gly	Asn	Ser	Leu	Pro	Glu	Arg	Asn	Ser	Glu
				725					730					735	
Lys	Ser	Asn	Ser	Leu	Asp	Lys	His	Gln	Gln	Ser	Ser	Thr	Leu	Gly	Asn
			740					745					750		
Ser	Val	Val	Arg	Cys	Asp	Lys	Leu	Asp	Gln	Ser	Glu	Ile	Lys	Ser	Leu
	755					760					765				
Leu	Met	Cys	Phe	Leu	Tyr	Ile	Leu	Lys	Ser	Met	Ser	Asp	Asp	Ala	Leu
	770				775						780				
Phe	Thr	Tyr	Trp	Asn	Lys	Ala	Ser	Thr	Ser	Glu	Leu	Met	Asp	Phe	Phe
785				790						795					800
Thr	Ile	Ser	Glu	Val	Cys	Leu	His	Gln	Phe	Gln	Tyr	Met	Gly	Lys	Arg
				805					810					815	
Tyr	Ile	Ala	Arg	Thr	Gly	Met	Met	His	Ala	Arg	Leu	Gln	Gln	Leu	Gly
			820					825					830		
Ser	Leu	Asp	Asn	Ser	Leu	Thr	Phe	Asn	His	Ser	Tyr	Gly	His	Ser	Asp
		835					840					845			
Ala	Asp	Val	Leu	His	Gln	Ser	Leu	Leu	Glu	Ala	Asn	Ile	Ala	Thr	Glu
	850					855					860				
Val	Cys	Leu	Thr	Ala	Leu	Asp	Thr	Leu	Ser	Leu	Phe	Thr	Leu	Ala	Phe
865				870						875				880	
Lys	Asn	Gln	Leu	Leu	Ala	Asp	His	Gly	His	Asn	Pro	Leu	Met	Lys	Lys
			885					890					895		
Val	Phe	Asp	Val	Tyr	Leu	Cys	Phe	Leu	Gln	Lys	His	Gln	Ser	Glu	Thr
		900						905					910		
Ala	Leu	Lys	Asn	Val	Phe	Thr	Ala	Leu	Arg	Ser	Leu	Ile	Tyr	Lys	Phe
	915						920					925			
Pro	Ser	Thr	Phe	Tyr	Glu	Gly	Arg	Ala	Asp	Met	Cys	Ala	Ala	Leu	Cys
	930					935					940				
Tyr	Glu	Ile	Leu	Lys	Cys	Cys	Asn	Ser	Lys	Leu	Ser	Ser	Ile	Arg	Thr
945				950						955				960	
Glu	Ala	Ser	Gln	Leu	Leu	Tyr	Phe	Leu	Met	Arg	Asn	Asn	Phe	Asp	Tyr
			965						970					975	
Thr	Gly	Lys	Lys	Ser	Phe	Val	Arg	Thr	His	Leu	Gln	Val	Ile	Ile	Ser
			980					985					990		

Val Ser Gln Leu Ile Ala Asp Val Val Gly Ile Gly Gly Thr Arg Phe  
 995 1000 1005  
 Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys Ala Asn Ser Asp Arg Leu  
 1010 1015 1020  
 Ile Lys His Thr Ser Phe Ser Ser Asp Val Lys Asp Leu Thr Lys Arg  
 1025 1030 1035 1040  
 Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met Lys Glu His Glu Asn  
 1045 1050 1055  
 Asp Pro Glu Met Leu Val Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr  
 1060 1065 1070  
 Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu Asp Ser Met Ala Arg  
 1075 1080 1085  
 Ile His Val Lys Asn Gly Asp Leu Ser Glu Ala Ala Met Cys Tyr Val  
 1090 1095 1100  
 His Val Thr Ala Leu Val Ala Glu Tyr Leu Thr Arg Lys Glu Ala Val  
 1105 1110 1115 1120  
 Gln Trp Glu Pro Pro Leu Leu Pro His Ser His Ser Ala Cys Leu Arg  
 1125 1130 1135  
 Arg Ser Arg Gly Gly Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val  
 1140 1145 1150  
 Ile Thr Pro Asn Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly  
 1155 1160 1165  
 Met Gln Asp Val His Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu  
 1170 1175 1180  
 Gln Cys Ala Asp Gly Leu Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala  
 1185 1190 1195 1200  
 Asp Ile Tyr Lys Leu Ile Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe  
 1205 1210 1215  
 Glu Arg Leu Ala His Leu Tyr Asp Thr Leu His Arg Ala Tyr Ser Lys  
 1220 1225 1230  
 Val Thr Glu Val Met His Ser Gly Arg Arg Leu Leu Gly Thr Tyr Phe  
 1235 1240 1245  
 Arg Val Ala Phe Phe Gly Gln Ala Ala Gln Tyr Gln Phe Thr Asp Ser  
 1250 1255 1260  
 Glu Thr Asp Val Glu Gly Phe Phe Glu Asp Glu Asp Gly Lys Glu Tyr  
 1265 1270 1275 1280  
 Ile Tyr Lys Glu Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg  
 1285 1290 1295  
 Leu Leu Lys Leu Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met  
 1300 1305 1310

Ile Gln Asp Ser Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Tyr  
 1315 1320 1325

Ala Tyr Ile Gln Val Thr His Val Ile Pro Phe Phe Asp Glu Lys Glu  
 1330 1335 1340

Leu Gln Glu Arg Lys Thr Glu Phe Glu Arg Ser His Asn Ile Arg Arg  
 1345 1350 1355 1360

Phe Met Phe Glu Met Pro Phe Thr Gln Thr Gly Lys Arg Gln Gly Gly  
 1365 1370 1375

Val Glu Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr Ala Ile His Cys  
 1380 1385 1390

Phe Pro Tyr Val Lys Lys Arg Ile Pro Val Met Tyr Gln His His Thr  
 1395 1400 1405

Asp Leu Asn Pro Ile Glu Val Ala Ile Asp Glu Met Ser Lys Lys Val  
 1410 1415 1420

Ala Glu Leu Arg Gln Leu Cys Ser Ser Ala Glu Val Asp Met Ile Lys  
 1425 1430 1435 1440

Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala Gly  
 1445 1450 1455

Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys Arg  
 1460 1465 1470

Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln Phe  
 1475 1480 1485

Val Glu Ala Cys Gly Gln Ala Leu Ala Val Asn Glu Arg Leu Ile Lys  
 1490 1495 1500

Glu Asp Gln Leu Glu Tyr Gln Glu Glu Met Lys Ala Asn Tyr Arg Glu  
 1505 1510 1515 1520

Met Ala Lys Glu Leu Ser Glu Ile Met His Glu Gln Leu Gly  
 1525 1530

<210> 11

<211> 738

<212> PRT

<213> Rattus norvegicus

<220>

<223> rat TRG

<400> 11

Lys Leu Ser Arg Gly His Ser Pro Leu Met Lys Lys Val Phe Asp Val  
 1 5 10 15

Tyr Leu Cys Phe Leu Gln Lys His Gln Ser Glu Met Ala Leu Lys Asn  
 20 25 30

Val Phe Thr Ala Leu Arg Ser Leu Ile Tyr Lys Phe Pro Ser Thr Phe  
 35 40 45

Tyr Glu Gly Arg Ala Asp Met Cys Ala Ser Leu Cys Tyr Glu Val Leu  
 50 55 60  
 Lys Cys Cys Asn Ser Lys Leu Ser Ser Ile Arg Thr Glu Ala Ser Gln  
 65 70 75 80  
 Leu Leu Tyr Phe Leu Met Arg Asn Asn Phe Asp Tyr Thr Gly Lys Lys  
 85 90 95  
 Ser Phe Val Arg Thr His Leu Gln Val Ile Ile Ser Leu Ser Gln Leu  
 100 105 110  
 Ile Ala Asp Val Val Gly Ile Gly Gly Thr Arg Phe Gln Gln Ser Leu  
 115 120 125  
 Ser Ile Ile Asn Asn Cys Ala Asn Ser Asp Arg Leu Ile Lys His Thr  
 130 135 140  
 Ser Phe Ser Ser Asp Val Lys Asp Leu Thr Lys Arg Ile Arg Thr Val  
 145 150 155 160  
 Leu Met Ala Thr Ala Gln Met Lys Glu His Glu Asn Asp Pro Glu Met  
 165 170 175  
 Leu Val Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr Ala Ser Thr Pro  
 180 185 190  
 Glu Leu Arg Lys Thr Trp Leu Asp Ser Met Ala Arg Ile His Val Lys  
 195 200 205  
 Asn Gly Asp Leu Ser Glu Ala Ala Met Cys Tyr Val His Val Thr Ala  
 210 215 220  
 Leu Val Ala Glu Tyr Leu Thr Arg Lys Glu Ala Asp Leu Ala Leu Gln  
 225 230 235 240  
 Arg Glu Pro Pro Val Phe Pro Tyr Ser His Thr Ser Cys Gln Arg Lys  
 245 250 255  
 Ser Arg Gly Gly Met Phe Arg Gln Gly Cys Thr Ala Phe Arg Val Ile  
 260 265 270  
 Thr Pro Asn Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly Met  
 275 280 285  
 Gln Asp Val His Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu Gln  
 290 295 300  
 Cys Ala Asp Gly Leu Trp Lys Ala Glu Arg Leu Arg Ala Gly Leu Leu  
 305 310 315 320  
 Thr Ser Ile Asn Ser Ser Ser Pro Ser Met Lys Ser Gly Gly Thr Leu  
 325 330 335  
 Glu Thr Thr His Leu Tyr Asp Thr Leu His Arg Pro Tyr Ser Lys Val  
 340 345 350  
 Thr Glu Val Ile Thr Arg Ala Ala Gly Ser Trp Asp Leu Leu Pro Gly  
 355 360 365  
 Gly Leu Phe Gly Gln Gly Phe Phe Glu Asp Glu Asp Gly Lys Glu Tyr

370	375	380
Ile Tyr Lys Glu Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg		
385	390	395 400
Leu Leu Lys Leu Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met		
	405	410 415
Ile Gln Asp Ser Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Phe		
	420	425 430
Ala Tyr Ile Gln Val Thr His Val Thr Pro Phe Phe Asp Glu Lys Glu		
	435	440 445
Leu Gln Glu Arg Lys Thr Glu Phe Glu Arg Cys His Asn Ile Arg Arg		
	450	455 460
Phe Met Phe Glu Met Pro Phe Thr Gln Thr Gly Lys Arg Gln Gly Gly		
	465	470 475 480
Val Glu Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr Ala Ile His Cys		
	485	490 495
Phe Pro Tyr Val Lys Lys Arg Ile Pro Val Met Tyr Gln His His Thr		
	500	505 510
Asp Leu Asn Pro Ile Glu Val Ala Ile Asp Glu Met Ser Lys Lys Val		
	515	520 525
Ala Glu Leu His Gln Leu Cys Ser Ser Ala Glu Val Asp Met Ile Lys		
	530	535 540
Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala Gly		
	545	550 555 560
Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys Arg		
	565	570 575
Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln Phe		
	580	585 590
Val Glu Ala Cys Gly Gln Ala Leu Ala Val Asn Glu Arg Leu Ile Lys		
	595	600 605
Glu Asp Gln Leu Glu Tyr Gln Glu Glu Met Lys Ala Asn Tyr Arg Glu		
	610	615 620
Ile Arg Lys Glu Leu Ser Asp Ile Ile Val Pro Arg Ile Cys Pro Gly		
	625	630 635 640
Glu Asp Lys Arg Ala Thr Lys Phe Pro Ala His Leu Gln Arg His Gln		
	645	650 655
Arg Asp Thr Asn Lys His Ser Gly Ser Arg Val Asp Gln Phe Ile Leu		
	660	665 670
Ser Cys Val Thr Leu Pro His Glu Pro His Val Gly Thr Cys Phe Val		
	675	680 685
Met Cys Lys Leu Arg Thr Thr Phe Arg Ala Asn His Trp Phe Cys Gln		
	690	695 700

Ala Gln Glu Glu Ala Met Gly Asn Gly Arg Glu Lys Glu Pro Trp Thr  
705 710 715 720

Val Ile Phe Asn Ser Arg Phe Tyr Arg Ser Trp Gly Lys Val His Ile  
725 730 735

Phe Phe

<210> 12

<211> 1214

<212> PRT

<213> Homo sapiens

<220>

<223> human CLASP-4

<400> 12

Met Glu Ile Gln Val Leu Ile Arg Phe Leu Ser Val Ile Leu Met Gln  
1 5 10 15

Leu Phe Trp Val Leu Pro Asn Met Ile His Glu Asp Asp Val Pro Ile  
20 25 30

Ser Cys Pro Met Val Leu Phe His Ile Val Ser Lys Cys His Glu Glu  
35 40 45

Gly Leu Asp Ser Tyr Leu Ser Ser Phe Ile Lys Tyr Ser Phe Arg Pro  
50 55 60

Gly Lys Pro Ser Ala Pro Gln Ala Pro Leu Ile His Glu Thr Leu Ala  
65 70 75 80

Thr Met Met Ile Ala Leu Leu Lys Gln Ser Ala Asp Phe Leu Ala Ile  
85 90 95

Asn Lys Leu Leu Lys Tyr Ser Trp Phe Phe Phe Glu Ile Ile Ala Lys  
100 105 110

Ser Met Ala Thr Tyr Leu Leu Glu Glu Asn Lys Ile Lys Leu Thr His  
115 120 125

Gly Gln Arg Phe Pro Lys Ala Tyr His His Ala Leu His Ser Leu Phe  
130 135 140

Leu Ala Ile Thr Ile Val Glu Ser Gln Tyr Ala Glu Ile Pro Lys Glu  
145 150 155 160

Ser Arg Asn Val Asn Tyr Ser Leu Ala Ser Phe Leu Lys Cys Cys Leu  
165 170 175

Thr Leu Met Asp Arg Gly Phe Val Phe Asn Leu Ile Asn Asp Tyr Ile  
180 185 190

Ser Gly Phe Ser Pro Lys Asp Pro Lys Val Leu Ala Glu Tyr Lys Phe  
195 200 205

Glu Phe Leu Gln Thr Ile Cys Asn His Glu His Tyr Ile Pro Leu Asn  
210 215 220

Leu Pro Met Ala Phe Ala Lys Pro Lys Leu Gln Arg Val Gln Asp Ser  
 225 230 235 240  
 Asn Leu Glu Tyr Ser Leu Ser Asp Glu Tyr Cys Lys His His Phe Leu  
 245 250 255  
 Val Gly Leu Leu Leu Arg Glu Thr Ser Ile Ala Leu Gln Asp Asn Tyr  
 260 265 270  
 Glu Ile Arg Tyr Thr Ala Ile Ser Val Ile Lys Asn Leu Leu Ile Lys  
 275 280 285  
 His Ala Phe Asp Thr Arg Tyr Gln His Lys Asn Gln Gln Ala Lys Ile  
 290 295 300  
 Ala Gln Leu Tyr Leu Pro Phe Val Gly Leu Leu Leu Glu Asn Ile Gln  
 305 310 315 320  
 Arg Leu Ala Gly Arg Asp Thr Leu Tyr Ser Cys Ala Ala Met Pro Asn  
 325 330 335  
 Ser Ala Ser Arg Asp Glu Phe Pro Cys Gly Phe Thr Ser Pro Ala Asn  
 340 345 350  
 Arg Gly Ser Leu Ser Thr Asp Lys Asp Thr Ala Tyr Gly Ser Phe Gln  
 355 360 365  
 Asn Gly His Gly Ile Lys Arg Glu Asp Ser Arg Gly Ser Leu Ile Pro  
 370 375 380  
 Glu Gly Ala Thr Gly Phe Pro Asp Gln Gly Asn Thr Gly Glu Asn Thr  
 385 390 395 400  
 Arg Gln Ser Ser Thr Arg Ser Ser Val Ser Gln Tyr Asn Arg Leu Asp  
 405 410 415  
 Gln Tyr Glu Ile Arg Ser Leu Leu Met Cys Tyr Leu Tyr Ile Val Lys  
 420 425 430  
 Met Ile Ser Glu Asp Thr Leu Leu Thr Tyr Trp Asn Lys Val Ser Pro  
 435 440 445  
 Gln Glu Leu Ile Asn Ile Leu Ile Leu Leu Glu Val Cys Leu Phe His  
 450 455 460  
 Phe Arg Tyr Met Gly Lys Arg Asn Ile Ala Arg Val His Asp Ala Trp  
 465 470 475 480  
 Leu Ser Lys His Phe Gly Ile Asp Arg Lys Ser Gln Thr Met Pro Ala  
 485 490 495  
 Leu Arg Asn Arg Ser Gly Val Met Gln Ala Arg Leu Gln His Leu Ser  
 500 505 510  
 Ser Leu Glu Ser Ser Phe Thr Leu Asn His Ser Ser Thr Thr Thr Glu  
 515 520 525  
 Ala Asp Ile Phe His Gln Ala Leu Leu Glu Gly Asn Thr Ala Thr Glu  
 530 535 540  
 Val Ser Leu Thr Val Leu Asp Thr Ile Ser Phe Phe Thr Gln Cys Phe



545		550		555		560
Lys Thr His Phe Leu Asn Asn Asp Gly His Asn Pro Leu Met Lys Lys						
	565			570		575
Val Phe Asp Ile His Leu Ala Phe Leu Lys Asn Gly Gln Ser Glu Val						
	580		585		590	
Ser Leu Lys His Val Phe Ala Ser Leu Arg Ala Phe Ile Ser Lys Phe						
	595	600		605		
Pro Ser Ala Phe Phe Lys Gly Arg Val Asn Met Cys Ala Ala Phe Cys						
	610	615		620		
Tyr Glu Val Leu Lys Cys Cys Thr Ser Lys Ile Ser Ser Thr Arg Asn						
625		630		635		640
Glu Ala Ser Ala Leu Leu Tyr Leu Leu Met Arg Asn Asn Phe Glu Tyr						
	645		650		655	
Thr Lys Arg Lys Thr Phe Leu Arg Thr His Leu Gln Ile Ile Ile Ala						
	660		665		670	
Val Ser Gln Leu Ile Ala Asp Val Ala Leu Ser Gly Gly Ser Arg Phe						
	675		680		685	
Gln Glu Ser Leu Phe Ile Ile Asn Asn Phe Ala Asn Ser Asp Arg Pro						
	690	695		700		
Met Leu Ala Arg Ala Phe Pro Ala Glu Val Lys Asp Leu Thr Lys Arg						
705		710		715		720
Ile Arg Thr Val Leu Met Ala Thr Ala Gln Met Lys Glu His Glu Lys						
	725		730		735	
Asp Pro Glu Met Leu Ile Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr						
	740		745		750	
Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp Leu Asp Ser Met Ala Lys						
	755		760		765	
Ile His Val Lys Asn Gly Asp Phe Ser Glu Ala Ala Met Cys Tyr Val						
	770	775		780		
His Val Ala Ala Leu Val Ala Glu Phe Leu His Arg Lys Lys Leu Phe						
785		790		795		800
Pro Asn Gly Cys Ser Ala Phe Lys Lys Ile Thr Pro Asn Ile Asp Glu						
	805		810		815	
Glu Gly Ala Met Lys Glu Asp Ala Gly Met Met Asp Val His Tyr Ser						
	820		825		830	
Glu Glu Val Leu Leu Glu Leu Leu Glu Gln Cys Val Asn Gly Leu Trp						
	835		840		845	
Lys Ala Glu Arg Tyr Glu Ile Ile Ser Glu Ile Ser Lys Leu Ile Gly						
	850	855		860		
Pro Ile Tyr Glu Asn Arg Arg Glu Phe Glu Asn Leu Thr Gln Val Tyr						
865		870		875		880

Arg Thr Leu His Gly Ala Tyr Thr Lys Ile Leu Glu Val Met His Thr  
 885 890 895  
 Lys Lys Arg Leu Leu Gly Thr Phe Phe Arg Val Ala Phe Tyr Gly Gln  
 900 905 910  
 Ser Phe Phe Glu Glu Glu Asp Gly Lys Glu Tyr Ile Tyr Lys Glu Pro  
 915 920 925  
 Lys Leu Thr Gly Leu Ser Glu Ile Ser Leu Arg Leu Val Lys Leu Tyr  
 930 935 940  
 Gly Glu Lys Phe Gly Thr Glu Asn Val Lys Ile Ile Gln Asp Ser Asp  
 945 950 955 960  
 Lys Val Asn Ala Lys Glu Leu Asp Pro Lys Tyr Ala His Ile Gln Val  
 965 970 975  
 Thr Tyr Val Lys Pro Tyr Phe Asp Asp Lys Glu Leu Thr Glu Arg Lys  
 980 985 990  
 Thr Glu Phe Glu Arg Asn His Asn Ile Ser Arg Phe Val Phe Glu Ala  
 995 1000 1005  
 Pro Tyr Thr Leu Ser Gly Lys Lys Gln Gly Cys Ile Glu Glu Gln Cys  
 1010 1015 1020  
 Lys Arg Arg Thr Ile Leu Thr Thr Ser Asn Ser Phe Pro Tyr Val Lys  
 1025 1030 1035 1040  
 Lys Arg Ile Pro Ile Asn Cys Glu Gln Gln Ile Asn Leu Lys Pro Ile  
 1045 1050 1055  
 Asp Gly Ala Thr Asp Glu Ile Lys Asp Lys Thr Ala Glu Leu Gln Lys  
 1060 1065 1070  
 Leu Cys Ser Ser Thr Asp Val Asp Met Ile Gln Leu Gln Leu Lys Leu  
 1075 1080 1085  
 Gln Gly Trp Val Ser Val Gln Val Asn Ala Gly Pro Leu Ala Tyr Ala  
 1090 1095 1100  
 Arg Ala Phe Leu Asn Asp Ser Gln Ala Ser Lys Tyr Pro Pro Lys Lys  
 1105 1110 1115 1120  
 Val Ser Glu Leu Lys Asp Met Phe Arg Lys Phe Ile Gln Ala Cys Ser  
 1125 1130 1135  
 Ile Ala Leu Glu Leu Asn Glu Arg Leu Ile Lys Glu Asp Gln Val Glu  
 1140 1145 1150  
 Tyr His Glu Gly Leu Lys Ser Asn Phe Arg Asp Met Val Lys Glu Leu  
 1155 1160 1165  
 Ser Asp Ile Ile His Glu Gln Ile Leu Gln Glu Asp Thr Met His Ser  
 1170 1175 1180  
 Pro Trp Met Ser Asn Thr Leu His Val Phe Cys Ala Ile Ser Gly Thr  
 1185 1190 1195 1200

Ser Ser Asp Arg Gly Tyr Gly Ser Pro Arg Tyr Ala Glu Val  
                   1205                  1210

<210> 13

<211> 1288

<212> PRT

<213> Homo sapiens

<220>

<223> human CLASP-1

<400> 13

Met Ser Phe Leu Pro Ile Ile Leu Asn Gln Leu Phe Lys Val Leu Val  
   1                  5                  10                  15

Gln Asn Glu Glu Asp Glu Ile Thr Thr Thr Val Thr Arg Val Leu Pro  
                   20                  25                  30

Asp Ile Val Ala Lys Cys His Glu Glu Gln Leu Asp His Ser Val Gln  
                   35                  40                  45

Ser Tyr Ile Lys Phe Val Phe Lys Thr Arg Ala Cys Lys Glu Arg Pro  
                   50                  55                  60

Val His Glu Asp Leu Ala Lys Asn Val Thr Gly Leu Leu Lys Ser Asn  
   65                  70                  75                  80

Asp Ser Pro Thr Val Lys His Val Leu Lys His Ser Trp Phe Phe Phe  
                   85                  90                  95

Ala Ile Ile Leu Lys Ser Met Ala Gln His Leu Ile Asp Thr Asn Lys  
                   100                  105                  110

Ile Gln Leu Pro Arg Pro Gln Arg Phe Pro Glu Ser Tyr Gln Asn Glu  
                   115                  120                  125

Leu Asp Asn Leu Val Met Val Leu Ser Asp His Val Ile Trp Lys Tyr  
                   130                  135                  140

Lys Asp Ala Leu Glu Glu Thr Arg Arg Ala Thr His Ser Val Ala Arg  
   145                  150                  155                  160

Phe Leu Lys Arg Cys Phe Thr Phe Met Asp Arg Gly Cys Val Phe Lys  
                   165                  170                  175

Met Val Asn Asn Tyr Ile Ser Met Phe Ser Ser Gly Asp Leu Lys Thr  
                   180                  185                  190

Leu Cys Gln Tyr Lys Phe Asp Phe Leu Gln Glu Val Cys Gln His Glu  
                   195                  200                  205

His Phe Ile Pro Leu Cys Leu Pro Ile Arg Ser Ala Asn Ile Pro Asp  
                   210                  215                  220

Pro Leu Thr Pro Ser Glu Ser Thr Gln Glu Leu His Ala Ser Asp Met  
   225                  230                  235                  240

Pro Glu Tyr Ser Val Thr Asn Glu Phe Cys Arg Lys His Phe Leu Ile  
                   245                  250                  255

Gly Ile Leu Leu Arg Glu Val Gly Phe Ala Leu Gln Glu Asp Gln Asp  
 260 265 270  
 Val Arg His Leu Ala Leu Ala Val Leu Lys Asn Leu Met Ala Lys His  
 275 280 285  
 Ser Phe Asp Asp Arg Tyr Arg Glu Pro Arg Lys Gln Ala Gln Ile Ala  
 290 295 300  
 Ser Leu Tyr Met Pro Leu Tyr Gly Met Leu Leu Asp Asn Met Pro Arg  
 305 310 315 320  
 Ile Tyr Leu Lys Asp Leu Tyr Pro Phe Thr Val Asn Thr Ser Asn Gln  
 325 330 335  
 Gly Ser Arg Asp Asp Leu Ser Thr Asn Gly Gly Phe Gln Ser Gln Thr  
 340 345 350  
 Ala Ile Lys His Ala Asn Ser Val Asp Thr Ser Phe Ser Lys Asp Val  
 355 360 365  
 Leu Asn Ser Ile Ala Ala Phe Ser Ser Ile Ala Ile Ser Thr Val Asn  
 370 375 380  
 His Ala Asp Ser Arg Ala Ser Leu Ala Ser Leu Asp Ser Asn Pro Ser  
 385 390 395 400  
 Thr Asn Glu Lys Ser Ser Glu Lys Thr Asp Asn Cys Glu Lys Ile Pro  
 405 410 415  
 Arg Pro Leu Ala Leu Ile Gly Ser Thr Leu Arg Phe Asp Arg Leu Asp  
 420 425 430  
 Gln Ala Glu Thr Arg Ser Leu Leu Met Cys Phe Leu His Ile Met Lys  
 435 440 445  
 Thr Ile Ser Tyr Glu Thr Leu Ile Ala Tyr Trp Gln Arg Ala Pro Ser  
 450 455 460  
 Pro Glu Val Ser Asp Phe Phe Ser Ile Leu Asp Val Cys Leu Gln Asn  
 465 470 475 480  
 Phe Arg Tyr Leu Gly Lys Arg Asn Ile Ile Arg Lys Ile Ala Ala Ala  
 485 490 495  
 Phe Lys Phe Val Gln Ser Thr Gln Asn Asn Gly Thr Leu Lys Gly Ser  
 500 505 510  
 Asn Pro Ser Cys Gln Thr Ser Gly Leu Leu Ala Gln Trp Met His Ser  
 515 520 525  
 Thr Ser Arg His Glu Gly His Lys Gln His Arg Ser Gln Thr Leu Pro  
 530 535 540  
 Ile Ile Arg Gly Lys Asn Ala Leu Ser Asn Pro Lys Leu Leu Gln Met  
 545 550 555 560  
 Leu Asp Asn Thr Met Thr Ser Asn Ser Asn Glu Ile Asp Ile Val His  
 565 570 575  
 His Val Asp Thr Glu Ala Asn Ile Ala Thr Glu Gly Cys Leu Thr Ile

580				585				590							
Leu	Asp	Leu	Val	Ser	Leu	Phe	Thr	Gln	Thr	His	Gln	Arg	Gln	Leu	Gln
	595						600					605			
Gln	Cys	Asp	Cys	Gln	Asn	Ser	Leu	Met	Lys	Arg	Gly	Phe	Asp	Thr	Tyr
	610					615					620				
Met	Leu	Phe	Phe	Gln	Val	Asn	Gln	Ser	Ala	Thr	Ala	Leu	Lys	His	Val
	625				630					635					640
Phe	Ala	Ser	Leu	Arg	Leu	Phe	Val	Cys	Lys	Phe	Pro	Ser	Ala	Phe	Phe
				645					650					655	
Gln	Gly	Pro	Ala	Asp	Leu	Cys	Gly	Ser	Phe	Cys	Tyr	Glu	Val	Leu	Lys
			660					665					670		
Cys	Cys	Asn	His	Arg	Ser	Arg	Ser	Thr	Gln	Thr	Glu	Ala	Ser	Ala	Leu
		675					680					685			
Leu	Tyr	Leu	Phe	Met	Arg	Lys	Asn	Phe	Glu	Phe	Asn	Lys	Gln	Lys	Ser
	690					695					700				
Ile	Val	Arg	Ser	His	Leu	Gln	Leu	Ile	Lys	Ala	Val	Ser	Gln	Leu	Ile
	705				710					715					720
Ala	Asp	Ala	Gly	Ile	Gly	Gly	Ser	Arg	Phe	Gln	His	Ser	Leu	Ala	Ile
				725					730					735	
Thr	Asn	Asn	Phe	Ala	Asn	Gly	Asp	Lys	Gln	Met	Lys	Asn	Ser	Asn	Phe
			740					745					750		
Pro	Ala	Glu	Val	Lys	Asp	Leu	Thr	Lys	Arg	Ile	Arg	Thr	Val	Leu	Met
		755					760					765			
Ala	Thr	Ala	Gln	Met	Lys	Glu	His	Glu	Lys	Asp	Pro	Glu	Met	Leu	Val
	770					775					780				
Asp	Leu	Gln	Tyr	Ser	Leu	Ala	Asn	Ser	Tyr	Ala	Ser	Thr	Pro	Glu	Leu
	785				790					795					800
Arg	Arg	Thr	Trp	Leu	Glu	Ser	Met	Ala	Lys	Ile	His	Ala	Arg	Asn	Gly
				805					810					815	
Asp	Leu	Ser	Glu	Ala	Ala	Met	Cys	Tyr	Ile	His	Ile	Ala	Ala	Leu	Ile
			820					825					830		
Ala	Glu	Tyr	Leu	Lys	Arg	Lys	Gly	Tyr	Trp	Lys	Val	Glu	Lys	Ile	Cys
		835					840					845			
Thr	Ala	Ser	Leu	Leu	Ser	Glu	Asp	Thr	His	Pro	Cys	Asp	Ser	Asn	Ser
	850					855					860				
Leu	Leu	Thr	Thr	Pro	Ser	Gly	Gly	Ser	Met	Phe	Ser	Met	Gly	Trp	Pro
	865				870					875					880
Ala	Phe	Leu	Ser	Ile	Thr	Pro	Asn	Ile	Lys	Glu	Glu	Gly	Ala	Ala	Lys
				885					890					895	
Glu	Asp	Ser	Gly	Met	His	Asp	Thr	Pro	Tyr	Asn	Glu	Asn	Ile	Leu	Val
			900					905					910		

Glu Gln Leu Tyr Met Cys Gly Glu Phe Leu Trp Lys Ser Glu Arg Tyr  
 915 920 925

Glu Leu Ile Ala Asp Val Asn Lys Pro Ile Ile Ala Val Phe Glu Lys  
 930 935 940

Gln Arg Asp Phe Lys Lys Leu Ser Asp Leu Tyr Tyr Asp Ile His Arg  
 945 950 955 960

Ser Tyr Leu Lys Val Ala Glu Val Val Asn Ser Glu Lys Arg Leu Phe  
 965 970 975

Gly Arg Tyr Tyr Arg Val Ala Phe Tyr Gly Gln Gly Phe Phe Glu Glu  
 980 985 990

Glu Glu Gly Lys Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr Gly Leu  
 995 1000 1005

Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu Tyr Ala Asp Lys Phe Gly  
 1010 1015 1020

Ala Asp Asn Val Lys Ile Ile Gln Asp Ser Asn Lys Val Asn Pro Lys  
 1025 1030 1035 1040

Asp Leu Asp Pro Lys Tyr Ala Tyr Ile Gln Val Thr Tyr Val Thr Pro  
 1045 1050 1055

Phe Phe Glu Glu Lys Glu Ile Glu Asp Arg Lys Thr Asp Phe Glu Met  
 1060 1065 1070

His His Asn Ile Asn Arg Phe Val Phe Glu Thr Pro Phe Thr Leu Ser  
 1075 1080 1085

Gly Lys Lys His Gly Gly Val Ala Glu Gln Cys Lys Arg Arg Thr Ile  
 1090 1095 1100

Leu Thr Thr Ser His Leu Phe Pro Tyr Val Lys Lys Arg Ile Gln Val  
 1105 1110 1115 1120

Ile Ser Gln Ser Ser Thr Glu Leu Asn Pro Ile Glu Val Ala Ile Asp  
 1125 1130 1135

Glu Met Ser Arg Lys Val Ser Glu Leu Asn Gln Leu Cys Thr Met Glu  
 1140 1145 1150

Glu Val Asp Met Ile Ser Leu Gln Leu Lys Leu Gln Gly Ser Val Ser  
 1155 1160 1165

Val Lys Val Asn Ala Gly Pro Met Ala Tyr Ala Arg Ala Phe Leu Glu  
 1170 1175 1180

Glu Thr Asn Ala Lys Lys Tyr Pro Asp Asn Gln Val Lys Leu Leu Lys  
 1185 1190 1195 1200

Glu Ile Phe Arg Gln Phe Ala Asp Ala Cys Gly Gln Ala Leu Asp Val  
 1205 1210 1215

Asn Glu Arg Leu Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu Glu Leu  
 1220 1225 1230

Arg Ser His Tyr Lys Asp Met Leu Ser Glu Leu Ser Thr Val Met Asn  
 1235 1240 1245

Glu Gln Ile Thr Gly Arg Asp Asp Leu Ser Lys Arg Gly Val Asp Gln  
 1250 1255 1260

Thr Cys Thr Arg Val Ile Ser Lys Ala Thr Pro Ala Leu Pro Thr Val  
 1265 1270 1275 1280

Ser Ile Ser Ser Ser Ala Glu Val  
 1285

<210> 14

<211> 1220

<212> PRT

<213> Homo sapiens

<220>

<223> human CLASP-3

<400> 14

Gly Pro Gly Pro Ala Arg Ser Thr Val Ser Ile Ser Leu Ile Ser Asn  
 1 5 10 15

Ser Ala Arg Val Asn Arg Ser Arg Ser Leu Ser Asn Ser Asn Pro Asp  
 20 25 30

Ile Ser Gly Thr Pro Thr Ser Pro Asp Asp Glu Val Arg Ser Ile Ile  
 35 40 45

Gly Ser Lys Gly Leu Asp Arg Ser Asn Ser Trp Val Asn Thr Gly Gly  
 50 55 60

Pro Lys Ala Ala Pro Trp Gly Ser Asn Pro Ser Pro Ser Ala Glu Ser  
 65 70 75 80

Thr Gln Ala Met Asp Arg Ser Cys Asn Arg Met Ser Ser His Thr Glu  
 85 90 95

Thr Ser Ser Phe Leu Gln Thr Leu Thr Gly Arg Leu Pro Thr Lys Lys  
 100 105 110

Leu Phe His Glu Glu Leu Ala Leu Gln Trp Val Val Cys Ser Gly Ser  
 115 120 125

Val Arg Glu Ser Ala Leu Gln Gln Ala Trp Phe Phe Phe Glu Leu Met  
 130 135 140

Val Lys Ser Met Val His His Leu Tyr Phe Asn Asp Lys Leu Glu Ala  
 145 150 155 160

Pro Arg Lys Ser Arg Phe Pro Glu Arg Phe Met Asp Asp Ile Ala Ala  
 165 170 175

Leu Val Ser Thr Ile Ala Ser Asp Ile Val Ser Arg Phe Gln Lys Asp  
 180 185 190

Thr Glu Met Val Glu Arg Leu Asn Thr Ser Leu Ala Phe Phe Leu Asn  
 195 200 205

Asp Leu Leu Ser Val Met Asp Arg Gly Phe Val Phe Ser Leu Ile Lys  
 210 215 220  
 Ser Cys Tyr Lys Gln Val Ser Ser Lys Leu Tyr Ser Leu Pro Asn Pro  
 225 230 235 240  
 Ser Val Leu Val Ser Leu Arg Leu Asp Phe Leu Arg Ile Ile Cys Ser  
 245 250 255  
 His Glu His Tyr Val Thr Leu Asn Leu Pro Cys Ser Leu Leu Thr Pro  
 260 265 270  
 Pro Ala Ser Pro Ser Pro Ser Val Ser Ser Ala Thr Ser Gln Ser Ser  
 275 280 285  
 Gly Phe Ser Thr Asn Val Gln Asp Gln Lys Ile Ala Asn Met Phe Glu  
 290 295 300  
 Leu Ser Val Pro Phe Arg Gln Gln His Tyr Leu Ala Gly Leu Val Leu  
 305 310 315 320  
 Thr Glu Leu Ala Val Ile Leu Asp Pro Asp Ala Glu Gly Leu Phe Gly  
 325 330 335  
 Leu His Lys Lys Val Ile Asn Met Val His Asn Leu Leu Ser Ser His  
 340 345 350  
 Asp Ser Asp Pro Arg Tyr Ser Asp Pro Gln Ile Lys Ala Arg Val Ala  
 355 360 365  
 Met Leu Tyr Leu Pro Leu Ile Gly Ile Ile Met Glu Thr Val Pro Gln  
 370 375 380  
 Leu Tyr Asp Phe Thr Glu Thr His Asn Gln Arg Gly Arg Pro Ile Cys  
 385 390 395 400  
 Ile Ala Thr Asp Asp Tyr Glu Ser Glu Ser Gly Ser Met Ile Ser Gln  
 405 410 415  
 Thr Val Ala Met Ala Ile Ala Gly Thr Ser Val Pro Gln Leu Thr Arg  
 420 425 430  
 Pro Gly Ser Phe Leu Leu Thr Ser Thr Ser Gly Arg Gln His Thr Thr  
 435 440 445  
 Phe Ser Ala Glu Ser Ser Arg Ser Leu Leu Ile Cys Leu Leu Trp Val  
 450 455 460  
 Leu Lys Asn Ala Asp Glu Thr Val Leu Gln Lys Trp Phe Thr Asp Leu  
 465 470 475 480  
 Ser Val Leu Gln Leu Asn Arg Leu Leu Asp Leu Leu Tyr Leu Cys Val  
 485 490 495  
 Ser Cys Phe Glu Tyr Lys Gly Lys Lys Val Phe Glu Arg Met Asn Ser  
 500 505 510  
 Leu Thr Phe Lys Lys Ser Lys Asp Met Arg Ala Lys Leu Glu Glu Ala  
 515 520 525  
 Ile Leu Gly Ser Ile Gly Ala Arg Gln Glu Met Val Arg Arg Ser Arg



530	535	540
Gly Gln Leu Glu Arg Ser Pro Ser Gly Ser Ala Phe Gly Ser Gln Glu 545 550 555 560		
Asn Leu Arg Trp Arg Lys Asp Met Thr His Trp Arg Gln Asn Thr Glu 565 570 575		
Lys Leu Asp Lys Ser Arg Ala Glu Ile Glu His Glu Ala Leu Ile Asp 580 585 590		
Gly Asn Leu Ala Thr Glu Ala Asn Leu Ile Ile Leu Asp Thr Leu Glu 595 600 605		
Ile Val Val Gln Thr Val Ser Val Thr Glu Ser Lys Glu Ser Ile Leu 610 615 620		
Gly Gly Val Leu Lys Val Leu Leu His Ser Met Ala Cys Asn Gln Ser 625 630 635 640		
Ala Val Tyr Leu Gln His Cys Phe Ala Thr Gln Arg Ala Leu Val Ser 645 650 655		
Lys Phe Pro Glu Leu Leu Phe Glu Glu Glu Thr Glu Gln Cys Ala Asp 660 665 670		
Leu Cys Leu Arg Leu Leu Arg His Cys Ser Ser Ser Ile Gly Thr Ile 675 680 685		
Arg Ser His Pro Ser Ala Ser Leu Tyr Leu Leu Met Arg Gln Asn Phe 690 695 700		
Glu Ile Gly Asn Asn Phe Ala Arg Val Lys Met Gln Val Pro Met Ser 705 710 715 720		
Leu Ser Ser Leu Val Gly Thr Ser Gln Asn Phe Asn Glu Glu Phe Leu 725 730 735		
Arg Arg Ser Leu Lys Thr Ile Leu Thr Tyr Ala Glu Glu Asp Leu Glu 740 745 750		
Leu Arg Glu Thr Thr Phe Pro Asp Gln Val Gln Asp Leu Val Phe Asn 755 760 765		
Leu His Met Ile Leu Ser Asp Thr Val Lys Met Lys Glu His Gln Glu 770 775 780		
Asp Pro Glu Met Leu Ile Asp Leu Met Tyr Arg Ile Ala Lys Gly Tyr 785 790 795 800		
Gln Thr Ser Pro Asp Leu Arg Leu Thr Trp Leu Gln Asn Met Ala Gly 805 810 815		
Lys His Ser Glu Arg Ser Asn His Ala Glu Ala Ala Gln Cys Leu Val 820 825 830		
His Ser Ala Ala Leu Val Ala Glu Tyr Leu Ser Met Leu Glu Asp Arg 835 840 845		
Lys Tyr Leu Pro Val Gly Cys Val Thr Phe Gln Asn Ile Ser Ser Asn 850 855 860		

Val	Leu	Glu	Glu	Ser	Ala	Val	Ser	Asp	Asp	Val	Val	Ser	Pro	Asp	Glu	865		870		875		880	
Glu	Gly	Ile	Cys	Ser	Gly	Lys	Tyr	Phe	Thr	Glu	Ser	Gly	Leu	Val	Gly		885		890			895	
Leu	Leu	Glu	Gln	Ala	Ala	Ala	Ser	Phe	Ser	Met	Ala	Gly	Met	Tyr	Glu		900		905			910	
Ala	Val	Asn	Glu	Val	Tyr	Lys	Val	Leu	Ile	Pro	Ile	His	Glu	Ala	Asn		915		920			925	
Arg	Asp	Ala	Lys	Lys	Leu	Ser	Thr	Ile	His	Gly	Lys	Leu	Gln	Glu	Ala		930		935			940	
Phe	Ser	Lys	Ile	Val	His	Gln	Ser	Thr	Gly	Trp	Glu	Arg	Met	Phe	Gly		945		950			955	960
Thr	Tyr	Phe	Arg	Val	Gly	Phe	Tyr	Gly	Thr	Lys	Phe	Gly	Asp	Leu	Asp		965		970				975
Glu	Gln	Glu	Phe	Val	Tyr	Lys	Glu	Pro	Ala	Ile	Thr	Lys	Leu	Ala	Glu		980		985				990
Ile	Ser	His	Arg	Leu	Glu	Gly	Phe	Tyr	Gly	Glu	Arg	Phe	Gly	Glu	Asp		995		1000			1005	
Val	Val	Glu	Val	Ile	Lys	Asp	Ser	Asn	Pro	Val	Asp	Lys	Cys	Lys	Leu		1010		1015			1020	
Asp	Pro	Asn	Lys	Ala	Tyr	Ile	Gln	Ile	Thr	Tyr	Val	Glu	Pro	Tyr	Phe		1025		1030			1035	1040
Asp	Thr	Tyr	Glu	Met	Lys	Asp	Arg	Ile	Thr	Tyr	Phe	Asp	Lys	Asn	Tyr		1045		1050				1055
Asn	Leu	Arg	Arg	Phe	Met	Tyr	Cys	Thr	Pro	Phe	Thr	Leu	Asp	Gly	Arg		1060		1065				1070
Ala	His	Gly	Glu	Leu	His	Glu	Gln	Phe	Lys	Arg	Lys	Thr	Ile	Leu	Thr		1075		1080				1085
Thr	Ser	His	Ala	Phe	Pro	Tyr	Ile	Lys	Thr	Arg	Val	Asn	Val	Thr	His		1090		1095			1100	
Lys	Glu	Glu	Ile	Ile	Leu	Thr	Pro	Ile	Glu	Val	Ala	Ile	Glu	Asp	Met		1105		1110			1115	1120
Gln	Lys	Lys	Thr	Gln	Glu	Leu	Ala	Phe	Ala	Thr	His	Gln	Asp	Pro	Ala		1125		1130				1135
Asp	Pro	Lys	Met	Leu	Gln	Met	Val	Leu	Gln	Gly	Ser	Val	Gly	Thr	Thr		1140		1145				1150
Val	Asn	Gln	Gly	Pro	Leu	Glu	Val	Ala	Gln	Val	Phe	Leu	Ser	Glu	Ile		1155		1160				1165
Pro	Ser	Asp	Pro	Lys	Leu	Phe	Arg	His	His	Asn	Lys	Leu	Arg	Leu	Cys		1170		1175				1180

Phe Lys Asp Phe Thr Lys Arg Cys Glu Asp Ala Leu Arg Lys Asn Lys  
 1185 1190 1195 1200

Ser Leu Ile Gly Pro Val Gln Lys Glu Tyr Gln Arg Glu Leu Gly Lys  
 1205 1210 1215

Leu Ser Ser Pro  
 1220

<210> 15

<211> 987

<212> PRT

<213> Homo sapiens

<220>

<223> human CLASP-5

<400> 15

Met Asn Ala Asp Thr Ala Pro Thr Ser Pro Cys Pro Ser Ile Ser Ser  
 1 5 10 15

Gln Asn Ser Ser Ser Cys Ser Ser Phe Gln Asp Gln Lys Ile Ala Ser  
 20 25 30

Met Phe Asp Arg Thr Ser Arg Val Pro Ala Ser Ser Thr Ser Ser Pro  
 35 40 45

Gly Leu Leu Phe Thr Glu Leu Ala Ala Ala Leu Asp Ala Glu Gly Glu  
 50 55 60

Gly Ile Ser Glu Val Gln Arg Lys Ala Val Ser Ala Ile His Ser Leu  
 65 70 75 80

Leu Ser Ser His Asp Leu Asp Pro Arg Cys Val Lys Pro Glu Val Lys  
 85 90 95

Val Lys Ile Ala Ala Leu Tyr Leu Pro Leu Val Gly Ile Ile Leu Asp  
 100 105 110

Ala Leu Pro Gln Leu Cys Asp Phe Thr Val Ala Asp Thr Arg Arg Tyr  
 115 120 125

Arg Thr Ser Gly Ser Asp Glu Glu Gln Glu Gly Ala Gly Ala Ile Thr  
 130 135 140

Gln Asn Val Ala Leu Ala Ile Ala Gly Asn Asn Phe Asn Leu Lys Thr  
 145 150 155 160

Ser Gly Ile Val Leu Ser Ser Leu Pro Tyr Lys Gln Tyr Asn Met Leu  
 165 170 175

Asn Ala Asp Thr Thr Arg Asn Leu Met Ile Cys Phe Leu Trp Ile Met  
 180 185 190

Lys Asn Ala Asp Gln Ser Leu Ile Arg Lys Trp Ile Ala Asp Leu Pro  
 195 200 205

Ser Thr Gln Leu Asn Arg Ile Leu Asp Leu Leu Phe Ile Cys Val Leu  
 210 215 220

Cys Phe Glu Tyr Lys Gly Lys Gln Ser Ser Asp Lys Val Ser Thr Gln  
 225 230 235 240  
 Val Leu Gln Lys Ser Arg Asp Val Lys Ala Arg Leu Glu Glu Ala Leu  
 245 250 255  
 Leu Arg Gly Glu Gly Ala Arg Gly Glu Met Met Arg Arg Arg Ala Pro  
 260 265 270  
 Gly Asn Asp Arg Phe Pro Gly Leu Asn Glu Asn Leu Arg Trp Lys Lys  
 275 280 285  
 Glu Gln Thr His Trp Arg Gln Ala Asn Glu Lys Leu Asp Lys Thr Lys  
 290 295 300  
 Ala Glu Leu Asp Gln Glu Ala Leu Ile Ser Gly Asn Leu Ala Thr Glu  
 305 310 315 320  
 Ala His Leu Ile Ile Leu Asp Met Gln Glu Asn Ile Ile Gln Ala Ser  
 325 330 335  
 Ser Ala Leu Asp Cys Lys Asp Ser Leu Leu Gly Gly Val Leu Arg Val  
 340 345 350  
 Leu Val Asn Ser Leu Asn Cys Asp Gln Ser Thr Thr Tyr Leu Thr His  
 355 360 365  
 Cys Phe Ala Thr Leu Arg Ala Leu Ile Ala Lys Phe Gly Asp Leu Leu  
 370 375 380  
 Phe Glu Glu Glu Val Glu Gln Cys Phe Asp Leu Cys His Gln Val Leu  
 385 390 395 400  
 His His Cys Ser Ser Ser Met Asp Val Thr Arg Ser Gln Ala Cys Ala  
 405 410 415  
 Thr Leu Tyr Leu Leu Met Arg Phe Ser Phe Gly Ala Thr Ser Asn Phe  
 420 425 430  
 Ala Arg Val Lys Met Gln Val Thr Met Ser Leu Ala Ser Leu Val Gly  
 435 440 445  
 Arg Ala Pro Asp Phe Asn Glu Glu His Leu Arg Arg Ser Leu Arg Thr  
 450 455 460  
 Ile Leu Ala Tyr Ser Glu Glu Asp Thr Ala Met Gln Met Thr Pro Phe  
 465 470 475 480  
 Pro Thr Gln Val Glu Glu Leu Leu Cys Asn Leu Asn Ser Ile Leu Tyr  
 485 490 495  
 Asp Thr Val Lys Met Arg Glu Phe Gln Glu Asp Pro Glu Met Leu Met  
 500 505 510  
 Asp Leu Met Tyr Arg Ile Ala Lys Ser Tyr Gln Ala Ser Pro Asp Leu  
 515 520 525  
 Arg Leu Thr Trp Leu Gln Asn Met Ala Glu Lys His Thr Lys Lys Lys  
 530 535 540  
 Cys Tyr Thr Glu Ala Ala Met Cys Leu Val His Ala Ala Ala Leu Val

545		550		555		560
Ala Glu Tyr Leu Ser Met Leu Glu Asp His Ser Tyr Leu Pro Val Gly						
	565		570		575	
Ser Val Ser Phe Gln Asn Ile Ser Ser Asn Val Leu Glu Glu Ser Val						
	580		585		590	
Val Ser Glu Asp Thr Leu Ser Pro Asp Glu Asp Gly Val Cys Ala Gly						
	595		600		605	
Gln Tyr Phe Thr Glu Ser Gly Leu Val Gly Leu Leu Glu Gln Ala Ala						
	610		615		620	
Glu Leu Phe Ser Thr Gly Gly Leu Tyr Glu Thr Val Asn Glu Val Tyr						
	625		630		635	640
Lys Leu Val Ile Pro Ile Leu Glu Ala His Arg Glu Phe Arg Lys Leu						
	645		650		655	
Thr Leu Thr His Ser Lys Leu Gln Arg Ala Phe Asp Ser Ile Val Asn						
	660		665		670	
Lys Asp His Lys Arg Met Phe Gly Thr Tyr Phe Arg Val Gly Phe Phe						
	675		680		685	
Gly Ser Lys Phe Gly Asp Leu Asp Glu Gln Glu Phe Val Tyr Lys Glu						
	690		695		700	
Pro Ala Ile Thr Lys Leu Pro Glu Ile Ser His Arg Leu Glu Ala Phe						
	705		710		715	720
Tyr Gly Gln Cys Phe Gly Ala Glu Phe Val Glu Val Ile Lys Asp Ser						
	725		730		735	
Thr Pro Val Asp Lys Thr Lys Leu Asp Pro Asn Lys Ala Tyr Ile Gln						
	740		745		750	
Ile Thr Phe Val Glu Pro Tyr Phe Asp Glu Tyr Glu Met Lys Asp Arg						
	755		760		765	
Val Thr Tyr Phe Glu Lys Asn Phe Asn Leu Arg Arg Phe Met Tyr Thr						
	770		775		780	
Thr Pro Phe Thr Leu Glu Gly Arg Pro Arg Gly Glu Leu His Glu Gln						
	785		790		795	800
Tyr Arg Arg Asn Thr Val Leu Thr Thr Met His Ala Phe Pro Tyr Ile						
	805		810		815	
Lys Thr Arg Ile Ser Val Ile Gln Lys Glu Glu Phe Val Leu Thr Pro						
	820		825		830	
Ile Glu Val Ala Ile Glu Asp Met Lys Lys Lys Thr Leu Gln Leu Ala						
	835		840		845	
Val Ala Ile Asn Gln Glu Pro Pro Asp Ala Lys Met Leu Gln Met Val						
	850		855		860	
Leu Gln Gly Ser Val Gly Ala Thr Val Asn Gln Gly Pro Leu Glu Val						
	865		870		875	880

Ala Gln Val Phe Leu Ala Glu Ile Pro Ala Asp Pro Lys Leu Tyr Arg  
                                   885                                  890                                  895

His His Asn Lys Leu Arg Leu Cys Phe Lys Glu Phe Ile Met Arg Cys  
                                   900                                  905                                  910

Gly Glu Ala Val Glu Lys Asn Lys Arg Leu Ile Thr Ala Asp Gln Arg  
                                   915                                  920                                  925

Glu Tyr Gln Gln Glu Leu Lys Lys Asn Tyr Asn Lys Leu Lys Glu Asn  
                                   930                                  935                                  940

Leu Arg Pro Met Ile Glu Arg Lys Ile Pro Glu Leu Tyr Lys Pro Ile  
                                   945                                  950                                  955                                  960

Phe Arg Val Glu Ser Gln Lys Arg Asp Ser Phe His Arg Ser Ser Phe  
                                   965                                  970                                  975

Arg Lys Cys Glu Thr Gln Leu Ser Gln Gly Ser  
                                   980                                  985

<210> 16

<211> 24

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs A  
                                   and B from human CLASP-1

<400> 16

Tyr Arg Val Ala Phe Tyr Gly Gln Gly Phe Phe Glu Glu Glu Glu Gly  
   1                                  5                                  10                                  15

Lys Glu Tyr Ile Tyr Lys Glu Pro  
                                   20

<210> 17

<211> 38

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs A  
                                   and B from human KIAA1058

<400> 17

Phe Arg Val Ala Phe Phe Gly Gln Ala Ala Gln Tyr Gln Phe Thr Asp  
   1                                  5                                  10                                  15

Ser Glu Thr Asp Val Glu Gly Phe Phe Glu Asp Glu Asp Gly Lys Glu  
                                   20                                  25                                  30

Tyr Ile Tyr Lys Glu Pro  
                                   35

<210> 18

<211> 14  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:DOCK motif B  
 from human CLASP-2

<400> 18  
 Phe Glu Asp Glu Asp Gly Lys Glu Tyr Ile Tyr Lys Glu Pro  
           1                  5                  10

<210> 19  
 <211> 24  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:DOCK motifs A  
 and B from human CLASP-6

<400> 19  
 Phe Arg Val Ala Phe Phe Gly Gln Gly Phe Phe Glu Asp Glu Asp Gly  
           1                  5                  10                  15  
 Lys Glu Tyr Ile Tyr Lys Glu Pro  
                           20

<210> 20  
 <211> 24  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:DOCK motifs A  
 and B from human CLASP-4

<400> 20  
 Phe Arg Val Ala Phe Tyr Gly Gln Ser Phe Phe Glu Glu Glu Asp Gly  
           1                  5                  10                  15  
 Lys Glu Tyr Ile Tyr Lys Glu Pro  
                           20

<210> 21  
 <211> 31  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:DOCK motifs A  
 and B from canonical DOCK180

<400> 21  
 Phe Ala Val Gly Tyr Tyr Gly Gln Gly Phe Pro Thr Phe Leu Arg Gly  
           1                  5                  10                  15  
 Lys Val Phe Ile Tyr Arg Gly Lys Glu Tyr Glu Arg Arg Glu Asp

20

25

30

&lt;210&gt; 22

&lt;211&gt; 31

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:DOCK motifs A  
and B from canonical DOCK2

&lt;400&gt; 22

Phe Ala Val Gly Tyr Tyr Gly Gln Gly Phe Pro Ser Phe Leu Arg Asn  
1 5 10 15Lys Val Phe Ile Tyr Arg Gly Lys Glu Tyr Glu Arg Arg Glu Asp  
20 25 30

&lt;210&gt; 23

&lt;211&gt; 24

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:DOCK motifs A  
and B from canonical DOCK3

&lt;400&gt; 23

Phe Arg Val Gly Phe Tyr Gly Arg Lys Phe Pro Phe Phe Leu Arg Asn  
1 5 10 15Lys Glu Tyr Val Cys Arg Gly His  
20

&lt;210&gt; 24

&lt;211&gt; 24

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:DOCK motifs A  
and B from human KIAA0716

&lt;400&gt; 24

Phe Arg Val Gly Phe Tyr Gly Lys Lys Phe Pro Phe Phe Leu Arg Asn  
1 5 10 15Lys Glu Phe Val Cys Arg Gly His  
20

&lt;210&gt; 25

&lt;211&gt; 23

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

&lt;223&gt; Description of Artificial Sequence:DOCK motifs A



and B from human CLASP-3

<400> 25

Phe Arg Val Gly Phe Tyr Gly Thr Lys Phe Gly Asp Leu Asp Glu Gln  
1 5 10 15

Glu Phe Val Tyr Lys Glu Pro  
20

<210> 26

<211> 60

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motif C  
from rat TRG

<400> 26

Pro Lys Leu Thr Pro Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu  
1 5 10 15

Tyr Ser Asp Lys Phe Gly Ser Glu Asn Val Lys Met Ile Gln Asp Ser  
20 25 30

Gly Lys Val Asn Pro Lys Asp Leu Asp Ser Lys Phe Ala Tyr Ile Gln  
35 40 45

Val Thr His Val Thr Pro Phe Phe Asp Glu Lys Glu  
50 55 60

<210> 27

<211> 60

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motif C  
from human CLASP-1

<400> 27

Pro Lys Leu Thr Gly Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu  
1 5 10 15

Tyr Ala Asp Lys Phe Gly Ala Asp Asn Val Lys Ile Ile Gln Asp Ser  
20 25 30

Asn Lys Val Asn Pro Lys Asp Leu Asp Pro Lys Tyr Ala Tyr Ile Gln  
35 40 45

Val Thr Tyr Val Thr Pro Phe Phe Glu Glu Lys Glu  
50 55 60

<210> 28

<211> 60

<212> PRT

<213> Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:DOCK motif C  
from human CLASP-2

&lt;400&gt; 28

Pro	Lys	Leu	Thr	Pro	Leu	Ser	Glu	Ile	Ser	Gln	Arg	Leu	Leu	Lys	Leu
1				5					10					15	

Tyr	Ser	Asp	Lys	Phe	Gly	Ser	Glu	Asn	Val	Lys	Met	Thr	Gln	Asp	Ser
			20					25					30		

Gly	Lys	Val	Asn	Pro	Lys	Asp	Leu	Asp	Ser	Lys	Tyr	Ala	Tyr	Ile	Gln
		35					40					45			

Val	Thr	His	Val	Ile	Pro	Phe	Asp	Glu	Lys	Glu
	50					55				60

&lt;210&gt; 29

&lt;211&gt; 60

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:DOCK motif C  
from human CLASP-4

&lt;400&gt; 29

Pro	Lys	Leu	Thr	Gly	Leu	Ser	Glu	Ile	Ser	Leu	Arg	Leu	Val	Lys	Leu
1				5					10					15	

Tyr	Gly	Glu	Lys	Phe	Gly	Thr	Glu	Asn	Val	Lys	Ile	Ile	Gln	Asp	Ser
			20					25					30		

Asp	Lys	Val	Asn	Ala	Lys	Glu	Leu	Asp	Pro	Lys	Tyr	Ala	His	Ile	Gln
		35					40					45			

Val	Thr	Tyr	Val	Lys	Pro	Tyr	Phe	Asp	Asp	Lys	Glu
	50					55					60

&lt;210&gt; 30

&lt;211&gt; 60

&lt;212&gt; PRT

&lt;213&gt; Artificial Sequence

&lt;220&gt;

<223> Description of Artificial Sequence:DOCK motif C  
from human CLASP-3

&lt;400&gt; 30

Pro	Ala	Ile	Thr	Lys	Leu	Ala	Glu	Ile	Ser	His	Arg	Leu	Glu	Gly	Phe
1				5					10					15	

Tyr	Gly	Glu	Arg	Phe	Gly	Glu	Asp	Val	Val	Glu	Val	Ile	Lys	Asp	Ser
			20					25					30		

Asn	Pro	Val	Asp	Lys	Cys	Lys	Leu	Asp	Pro	Asn	Lys	Ala	Tyr	Ile	Gln
		35					40					45			

Ile	Thr	Tyr	Val	Glu	Pro	Tyr	Phe	Asp	Thr	Tyr	Glu
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

50

55

60

<210> 31  
 <211> 54  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:DOCK motif C  
 from human KIAA0716

<400> 31  
 His Asp Tyr Glu Arg Leu Glu Ala Phe Gln Gln Arg Met Leu Asn Glu  
 1 5 10 15  
 Phe Pro His Ala Ile Ala Met Gln His Ala Asn Gln Pro Asp Glu Thr  
 20 25 30  
 Ile Phe Gln Ala Glu Ala Gln Tyr Leu Gln Ile Tyr Ala Val Thr Pro  
 35 40 45  
 Ile Pro Glu Ser Gln Glu  
 50

<210> 32  
 <211> 54  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:DOCK motif C  
 from canonical DOCK3

<400> 32  
 His Asp Tyr Glu Arg Leu Glu Ala Phe Gln Gln Arg Met Leu Ser Glu  
 1 5 10 15  
 Phe Pro Gln Ala Val Ala Met Gln His Pro Asn His Pro Asp Asp Ala  
 20 25 30  
 Ile Leu Gln Cys Asp Ala Gln Tyr Leu Gln Ile Tyr Ala Val Thr Pro  
 35 40 45  
 Ile Pro Asp Tyr Val Asp  
 50

<210> 33  
 <211> 46  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:DOCK motif C  
 from canonical DOCK2

<400> 33  
 Phe Gln Met Gln Leu Met Thr Gln Phe Pro Asn Ala Glu Lys Met Asn  
 1 5 10 15

Thr Thr Ser Ala Pro Gly Asp Asp Val Lys Asn Ala Pro Gly Gln Tyr  
                   20                                  25                                  30

Ile Gln Cys Phe Thr Val Gln Pro Val Leu Asp Glu His Pro  
                   35                                  40                                  45

<210> 34

<211> 53

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motif C  
                   from canonical DOCK180

<400> 34

Glu Tyr Glu Arg Arg Glu Asp Phe Gln Met Gln Leu Met Thr Gln Phe  
           1                                  5                                  10                                  15

Pro Asn Ala Glu Lys Met Asn Thr Thr Ser Ala Pro Gly Asp Asp Val  
                   20                                  25                                  30

Lys Asn Ala Pro Gly Gln Tyr Ile Gln Cys Phe Thr Val Gln Pro Val  
                   35                                  40                                  45

Leu Asp Glu His Pro  
           50

<210> 35

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs D  
                   and E from human CLASP-1

<400> 35

Arg Thr Ile Leu Thr Thr Ser His Leu Phe Pro Tyr Val Lys Lys Arg  
           1                                  5                                  10                                  15

Ile Gln Val Ile Ser Gln Ser Ser Thr Glu Leu Asn Pro Ile Glu Val  
                   20                                  25                                  30

Ala Ile Asp Glu Met Ser Arg Lys Val Ser Glu Leu Asn  
                   35                                  40                                  45

<210> 36

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs D  
                   and E from rat TRG

<400> 36

Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg  
 1 5 10 15

Ile Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val  
 20 25 30

Ala Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu His  
 35 40 45

<210> 37

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs D  
 and E from human KIAA1058

<400> 37

Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg  
 1 5 10 15

Ile Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val  
 20 25 30

Ala Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg  
 35 40 45

<210> 38

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs D  
 and E from human CLASP-2

<400> 38

Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg  
 1 5 10 15

Ile Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val  
 20 25 30

Ala Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg  
 35 40 45

<210> 39

<211> 44

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs D  
 and E from human CLASP-6

<400> 39

Arg Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg

1                      5                      10                      15  
 Ile Pro Phe Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val  
                     20                      25                      30

His Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg  
                     35                      40

<210> 40  
 <211> 45  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:DOCK motifs D  
 and E from human CLASP-4

<400> 40  
 Arg Thr Ile Leu Thr Thr Ser Asn Ser Phe Pro Tyr Val Lys Lys Arg  
   1                      5                      10                      15

Ile Pro Ile Asn Cys Glu Gln Gln Ile Asn Leu Lys Pro Ile Asp Val  
                     20                      25                      30

Ala Thr Asp Glu Ile Lys Asp Lys Thr Ala Glu Leu Gln  
                     35                      40                      45

<210> 41  
 <211> 45  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:DOCK motifs D  
 and E from human CLASP-3

<400> 41  
 Lys Thr Ile Leu Thr Thr Ser His Ala Phe Pro Tyr Ile Lys Thr Arg  
   1                      5                      10                      15

Val Asn Val Thr His Lys Glu Glu Ile Ile Leu Thr Pro Ile Glu Val  
                     20                      25                      30

Ala Ile Glu Asp Met Gln Lys Lys Thr Gln Glu Leu Ala  
                     35                      40                      45

<210> 42  
 <211> 45  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:DOCK motifs D  
 and E from human CLASP-5

<400> 42  
 Asn Thr Val Leu Thr Thr Met His Ala Phe Pro Tyr Ile Lys Thr Arg  
   1                      5                      10                      15

Ile Ser Val Ile Gln Lys Glu Glu Phe Val Leu Thr Pro Ile Glu Val  
                   20                  25                  30

Ala Ile Glu Asp Met Lys Lys Lys Thr Leu Gln Leu Ala  
                   35                  40                  45

<210> 43

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs D  
           and E from human KIAA0716

<400> 43

Arg Thr Ser Leu Tyr Leu Val Gln Ser Leu Pro Gly Ile Ser Arg Trp  
   1                  5                  10                  15

Phe Glu Val Glu Lys Arg Glu Val Val Glu Met Ser Pro Leu Glu Asn  
                   20                  25                  30

Ala Ile Glu Val Leu Glu Asn Lys Asn Gln Gln Leu Lys  
                   35                  40                  45

<210> 44

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs D  
           and E from canonical DOCK2

<400> 44

Arg Thr Ser Phe Val Thr Ala Tyr Lys Leu Pro Gly Ile Leu Arg Trp  
   1                  5                  10                  15

Phe Glu Val Val His Met Ser Gln Thr Thr Ile Ser Pro Leu Glu Asn  
                   20                  25                  30

Ala Ile Glu Thr Met Ser Thr Ala Asn Glu Lys Ile Leu  
                   35                  40                  45

<210> 45

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs D  
           and E from canonical DOCK3

<400> 45

Arg Thr Thr Leu Thr Leu Thr His Ser Leu Pro Gly Ile Ser Arg Trp  
   1                  5                  10                  15

Phe Glu Val Glu Arg Arg Glu Leu Val Glu Val Ser Pro Leu Glu Asn  
                           20                          25                          30

Ala Ile Gln Val Val Glu Asn Lys Asn Gln Glu Leu Arg  
                           35                          40                          45

<210> 46

<211> 45

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs D  
                           and E from canonical DOCK180

<400> 46

Arg Thr Ser Phe Val Thr Ala Tyr Lys Leu Pro Gly Ile Leu Arg Trp  
           1                          5                          10                          15

Phe Glu Val Val His Met Ser Gln Thr Thr Ile Ser Pro Leu Glu Asn  
                           20                          25                          30

Ala Ile Glu Thr Met Ser Thr Ala Asn Glu Lys Ile Leu  
                           35                          40                          45

<210> 47

<211> 58

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs F  
                           and G from human CLASP-1

<400> 47

Ser Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Lys Val Asn Ala  
           1                          5                          10                          15

Gly Pro Met Ala Tyr Ala Arg Ala Phe Leu Glu Glu Thr Asn Ala Lys  
                           20                          25                          30

Lys Tyr Pro Asp Asn Gln Val Lys Leu Leu Lys Glu Ile Phe Arg Gln  
                           35                          40                          45

Phe Ala Asp Ala Cys Gly Gln Ala Leu Asp  
           50                          55

<210> 48

<211> 58

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs F  
                           and G from rat TRG

<400> 48

Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala



1                      5                      10                      15

Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys  
                             20                      25                      30

Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln  
                             35                      40                      45

Phe Val Glu Ala Cys Gly Gln Ala Leu Ala  
                             50                      55

<210> 49  
 <211> 58  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:DOCK motifs F  
                             and G from human KIAA1058

<400> 49

Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala  
   1                                      5                                      10                                      15

Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys  
                             20                      25                      30

Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln  
                             35                      40                      45

Phe Val Glu Ala Cys Gly Gln Ala Leu Ala  
                             50                      55

<210> 50  
 <211> 58  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:DOCK motifs F  
                             and G from human CLASP-2

<400> 50

Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala  
   1                                      5                                      10                                      15

Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys  
                             20                      25                      30

Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln  
                             35                      40                      45

Phe Val Glu Ala Cys Gly Gln Ala Leu Ala  
                             50                      55

<210> 51  
 <211> 58  
 <212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs F  
and G from human CLASP-6

<400> 51

Lys Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Gln Val Asn Ala  
1 5 10 15

Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asp Asp Thr Asn Thr Lys  
20 25 30

Arg Tyr Pro Asp Asn Lys Val Lys Leu Leu Lys Glu Val Phe Arg Gln  
35 40 45

Phe Val Glu Ala Cys Gly Gln Ala Leu Ala  
50 55

<210> 52

<211> 58

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs F  
and G from human CLASP-3

<400> 52

Met Leu Gln Met Val Leu Gln Gly Ser Val Gly Thr Thr Val Asn Gln  
1 5 10 15

Gly Pro Leu Glu Val Ala Gln Val Phe Leu Ser Glu Ile Pro Ser Asp  
20 25 30

Pro Lys Leu Phe Arg His His Asn Lys Leu Arg Leu Cys Phe Lys Asp  
35 40 45

Phe Thr Lys Arg Cys Glu Asp Ala Leu Arg  
50 55

<210> 53

<211> 58

<212> PRT

<213> Artificial Sequence

<220>

<223> Description of Artificial Sequence:DOCK motifs F  
and G from human CLASP-4

<400> 53

Gln Leu Gln Leu Lys Leu Gln Gly Cys Val Ser Val Gln Val Asn Ala  
1 5 10 15

Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asn Asp Ser Gln Ala Ser  
20 25 30

Lys Tyr Pro Pro Lys Lys Val Ser Glu Leu Lys Asp Met Phe Arg Lys  
35 40 45

Phe Ile Gln Ala Cys Ser Ile Ala Leu Glu  
50 55

<210> 54  
<211> 58  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:DOCK motifs F  
and G from human CLASP-5

<400> 54  
Met Leu Gln Met Val Leu Gln Gly Ser Val Gly Ala Thr Val Asn Gln  
1 5 10 15  
Gly Pro Leu Glu Val Ala Gln Val Phe Leu Ala Glu Ile Pro Ala Asp  
20 25 30  
Pro Lys Leu Tyr Arg His His Asn Lys Leu Arg Leu Cys Phe Lys Glu  
35 40 45  
Phe Ile Met Arg Cys Gly Glu Ala Val Glu  
50 55

<210> 55  
<211> 60  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:DOCK motifs F  
and G from human KIAA0716

<400> 55  
Pro Leu Thr Met Cys Leu Asn Gly Val Ile Asp Ala Ala Val Asn Gly  
1 5 10 15  
Gly Val Ser Arg Tyr Gln Glu Ala Phe Phe Val Lys Glu Tyr Ile Leu  
20 25 30  
Ser His Pro Glu Asp Gly Glu Lys Ile Ala Arg Leu Arg Glu Leu Met  
35 40 45  
Leu Glu Gln Ala Gln Ile Leu Glu Phe Gly Leu Ala  
50 55 60

<210> 56  
<211> 60  
<212> PRT  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:DOCK motifs F  
and G from canonical DOCK2

<400> 56

Pro Leu Ser Met Leu Leu Asn Gly Ile Val Asp Pro Ala Val Met Gly  
 1 5 10 15  
 Gly Phe Ala Lys Tyr Glu Lys Ala Phe Phe Thr Glu Glu Tyr Val Arg  
 20 25 30  
 Asp His Pro Glu Asp Gln Asp Lys Leu Thr His Leu Lys Asp Leu Ile  
 35 40 45  
 Ala Trp Gln Ile Pro Phe Leu Gly Ala Gly Ile Lys  
 50 55 60

<210> 57  
 <211> 60  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:DOCK motifs F  
 and G from canonical DOCK3

<400> 57  
 Leu Leu Ser Met Cys Leu Asn Gly Val Ile Asp Ala Ala Val Asn Gly  
 1 5 10 15  
 Gly Ile Ala Arg Tyr Gln Glu Ala Phe Phe Asp Lys Asp Tyr Ile Asn  
 20 25 30  
 Lys His Pro Gly Asp Ala Glu Lys Ile Thr Gln Leu Lys Glu Leu Met  
 35 40 45  
 Gln Glu Gln Val His Val Leu Gly Val Gly Leu Ala  
 50 55 60

<210> 58  
 <211> 60  
 <212> PRT  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:DOCK motifs F  
 and G from canonical DOCK180

<400> 58  
 Pro Leu Ser Met Leu Leu Asn Gly Ile Val Asp Pro Ala Val Met Gly  
 1 5 10 15  
 Gly Phe Ala Lys Tyr Glu Lys Ala Phe Phe Thr Glu Glu Tyr Val Arg  
 20 25 30  
 Asp His Pro Glu Ala His Glu Lys Ile Glu Lys Leu Lys Asp Leu Ile  
 35 40 45  
 Ala Trp Gln Ile Pro Phe Leu Ala Glu Gly Ile Arg  
 50 55 60

<210> 59  
 <211> 2149

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;223&gt; preliminary human CLASP-7 cDNA sequence

&lt;220&gt;

&lt;221&gt; CDS

&lt;222&gt; (2) .. (1933)

&lt;223&gt; human CLASP-7

&lt;400&gt; 59

c ctt tca gaa gcc cgg gag agc gtc ttg ggg gat ttg ctg aag gtt gtg 49  
 Leu Ser Glu Ala Arg Glu Ser Val Leu Gly Asp Leu Leu Lys Val Val  
           1                          5                          10                          15

ctg tac agc ctg ggc agt gcc cag agt gcc ctc ttc ttg cag cat ggc 97  
 Leu Tyr Ser Leu Gly Ser Ala Gln Ser Ala Leu Phe Leu Gln His Gly  
                           20                          25                          30

ctg gcc acc cag agg gcc ctt gtg tcc aag ttc ccg gag ctg ctg ttc 145  
 Leu Ala Thr Gln Arg Ala Leu Val Ser Lys Phe Pro Glu Leu Leu Phe  
                           35                          40                          45

gag gag gac acg gag ctg tgt gcc gac ctg tgc ctg agg ctc cta cga 193  
 Glu Glu Asp Thr Glu Leu Cys Ala Asp Leu Cys Leu Arg Leu Leu Arg  
           50                          55                          60

cac tgt ggc agc cgc atc agc acc atc cgc acg cac gcc agc gcc tcg 241  
 His Cys Gly Ser Arg Ile Ser Thr Ile Arg Thr His Ala Ser Ala Ser  
           65                          70                          75                          80

ctg tac ctg ctc atg cga cag aac ttc gag atc gcc cac aac ttt gcc 289  
 Leu Tyr Leu Leu Met Arg Gln Asn Phe Glu Ile Gly His Asn Phe Ala  
                           85                          90                          95

cgt gtg aag atg cag gtc acc atg tct ctc tcg tcc ctg gtg ggg acg 337  
 Arg Val Lys Met Gln Val Thr Met Ser Leu Ser Ser Leu Val Gly Thr  
                           100                          105                          110

acg cag aac ttc agt gaa gag cac ctg cga cgt tca ctc aaa acc atc 385  
 Thr Gln Asn Phe Ser Glu Glu His Leu Arg Arg Ser Leu Lys Thr Ile  
                           115                          120                          125

ctc acc tat gct gag gag gac atg ggg ctg cgg gac agc acc ttc gca 433  
 Leu Thr Tyr Ala Glu Glu Asp Met Gly Leu Arg Asp Ser Thr Phe Ala  
           130                          135                          140

gag cag gtc cag gac ctg atg ttc aac ctg cac atg atc ctg acg gac 481  
 Glu Gln Val Gln Asp Leu Met Phe Asn Leu His Met Ile Leu Thr Asp  
           145                          150                          155                          160

acg gtg aag atg aag gaa cac cag gag gac cct gag atg ctc atc gac 529  
 Thr Val Lys Met Lys Glu His Gln Glu Asp Pro Glu Met Leu Ile Asp  
                           165                          170                          175

ctc atg tac aga att gcc cgg ggc tac cag ggc tca ccg gac ctt cgg 577  
 Leu Met Tyr Arg Ile Ala Arg Gly Tyr Gln Gly Ser Pro Asp Leu Arg  
                           180                          185                          190

ctg acc tgg ttg cag aac atg gcc ggg aag cac gcg gag ctg ggc aac 625

Leu	Thr	Trp	Leu	Gln	Asn	Met	Ala	Gly	Lys	His	Ala	Glu	Leu	Gly	Asn		
		195					200					205					
cac	gcc	gag	gcc	gcc	cag	tgc	atg	gtg	cac	gcg	gcc	gcc	ctc	gtg	gct	673	
His	Ala	Glu	Ala	Ala	Gln	Cys	Met	Val	His	Ala	Ala	Ala	Leu	Val	Ala		
	210					215					220						
gag	tac	ctc	gcc	ctg	ctc	gag	gac	cac	cgc	cac	ctg	ccc	gtg	ggc	tgc	721	
Glu	Tyr	Leu	Ala	Leu	Leu	Glu	Asp	His	Arg	His	Leu	Pro	Val	Gly	Cys		
	225				230					235					240		
gtt	tcc	ttc	cag	aac	atc	tca	tcc	aat	gtg	cta	gag	gag	tcc	gcc	atc	769	
Val	Ser	Phe	Gln	Asn	Ile	Ser	Ser	Asn	Val	Leu	Glu	Glu	Ser	Ala	Ile		
			245						250					255			
tcc	gac	gac	atc	ctg	tcg	ccc	gac	gag	gag	ggc	ttc	tgc	tcc	ggg	aag	817	
Ser	Asp	Asp	Ile	Leu	Ser	Pro	Asp	Glu	Glu	Gly	Phe	Cys	Ser	Gly	Lys		
			260					265					270				
cac	ttc	act	gag	ctg	ggg	ctg	gta	ggg	ttg	ctg	gaa	cag	gca	gcc	ggc	865	
His	Phe	Thr	Glu	Leu	Gly	Leu	Val	Gly	Leu	Leu	Glu	Gln	Ala	Ala	Gly		
		275					280					285					
tac	ttc	acc	atg	ggc	ggg	ctc	tac	gag	gcg	gtg	aat	gag	gtc	tac	aag	913	
Tyr	Phe	Thr	Met	Gly	Gly	Leu	Tyr	Glu	Ala	Val	Asn	Glu	Val	Tyr	Lys		
		290				295					300						
aac	ctc	atc	ccc	atc	ctg	gaa	gcc	cac	cgt	gac	tac	aag	aag	ctg	gcc	961	
Asn	Leu	Ile	Pro	Ile	Leu	Glu	Ala	His	Arg	Asp	Tyr	Lys	Lys	Leu	Ala		
	305				310					315					320		
gcg	gtg	cac	ggc	aaa	ctg	cag	gag	gcc	ttc	acc	aag	atc	atg	cac	cag	1009	
Ala	Val	His	Gly	Lys	Leu	Gln	Glu	Ala	Phe	Thr	Lys	Ile	Met	His	Gln		
				325				330						335			
agt	tcc	ggc	tgg	gag	cgc	gtg	ttc	ggg	acg	tat	ttc	cgc	gtg	ggc	ttc	1057	
Ser	Ser	Gly	Trp	Glu	Arg	Val	Phe	Gly	Thr	Tyr	Phe	Arg	Val	Gly	Phe		
			340					345					350				
tac	ggc	gcc	cac	ttc	ggt	gac	ctg	gat	gag	cag	gag	ttt	gtg	tac	aag	1105	
Tyr	Gly	Ala	His	Phe	Gly	Asp	Leu	Asp	Glu	Gln	Glu	Phe	Val	Tyr	Lys		
		355				360						365					
gag	cca	tcg	atc	acg	aag	ctg	gca	gag	atc	tca	cac	cgg	ctg	gag	gag	1153	
Glu	Pro	Ser	Ile	Thr	Lys	Leu	Ala	Glu	Ile	Ser	His	Arg	Leu	Glu	Glu		
		370				375					380						
ttc	tac	acg	gag	aga	ttt	ggc	gac	gac	gtc	gtt	gag	att	atc	aaa	gac	1201	
Phe	Tyr	Thr	Glu	Arg	Phe	Gly	Asp	Asp	Val	Val	Glu	Ile	Ile	Lys	Asp		
					390					395				400			
tct	tac	cct	gtg	gac	aag	tcc	aag	ctt	gac	tca	caa	aag	gcc	tac	atc	1249	
Ser	Tyr	Pro	Val	Asp	Lys	Ser	Lys	Leu	Asp	Ser	Gln	Lys	Ala	Tyr	Ile		
				405				410						415			
cag	atc	acg	tat	gtg	gaa	cgc	tac	ttt	gat	acc	tac	gag	ctc	aag	gac	1297	
Gln	Ile	Thr	Tyr	Val	Glu	Pro	Tyr	Phe	Asp	Thr	Tyr	Glu	Leu	Lys	Asp		
			420				425					430					
cgg	gtg	acc	tac	ttt	gac	cgc	aac	tat	ggg	ctt	cgc	aca	ttc	ctg	ttc	1345	
Arg	Val	Thr	Tyr	Phe	Asp	Arg	Asn	Tyr	Gly	Leu	Arg	Thr	Phe	Leu	Phe		

435	440	445	
tgc acg ccg ttc acg ccg gat	ggg cgc gca cac	ggg gag ctg ccc gag	1393
Cys Thr Pro Phe Thr Pro Asp	Gly Arg Ala His	Gly Glu Leu Pro Glu	
450	455	460	
caa cac aag cgt aag acg ctg	ctc agc acc gac	cac gcc ttc ccc tac	1441
Gln His Lys Arg Lys Thr Leu	Leu Ser Thr Asp	His Ala Phe Pro Tyr	
465	470	475	480
atc aag act cgc atc cgt gtg	tgc cac cgg gag gag	acg gtg ctg acg	1489
Ile Lys Thr Arg Ile Arg Val	Cys His Arg Glu Glu	Thr Val Leu Thr	
485	490	495	
cca gtg gag gtg gcc atc gag	gac atg cag aag aag	aca cgg gag ctg	1537
Pro Val Glu Val Ala Ile Glu	Asp Met Gln Lys Lys	Thr Arg Glu Leu	
500	505	510	
gcc ttt gcc acc gag cag gac	cca cca gat gct aag	atg cta cag atg	1585
Ala Phe Ala Thr Glu Gln Asp	Pro Pro Asp Ala Lys	Met Leu Gln Met	
515	520	525	
gtg ctt cag ggc tct gta ggg	ccc acc gtg aac	cag ggt ccc ctg gag	1633
Val Leu Gln Gly Ser Val Gly	Pro Thr Val Asn	Gln Gly Pro Leu Glu	
530	535	540	
gtg gcc cag gtg ttt tta gca	gag atc ccg gaa gac	ccc aag ctc ttc	1681
Val Ala Gln Val Phe Leu Ala	Glu Ile Pro Glu Asp	Pro Lys Leu Phe	
545	550	555	560
cgg cat cac aac aaa ttg cgg	ctc tgc ttc aag gac	ttc tgc aag aaa	1729
Arg His His Asn Lys Leu Arg	Leu Cys Phe Lys Asp	Phe Cys Lys Lys	
565	570	575	
tgt gag gat gcg ctg cgg aaa	aat aag gcc ctg att	ggg ccg gac cag	1777
Cys Glu Asp Ala Leu Arg Lys	Asn Lys Ala Leu Ile	Gly Pro Asp Gln	
580	585	590	
aag gag tac cac cgt gag ctg	gag cgc aac tac tgc	cgc ctg cgg gag	1825
Lys Glu Tyr His Arg Glu Leu	Glu Arg Asn Tyr Cys	Arg Leu Arg Glu	
595	600	605	
gct ctg cag ccc ctg ctt acc	cag cgc ctg ccc	cag ctg atg gca ccc	1873
Ala Leu Gln Pro Leu Leu Thr	Gln Arg Leu Pro	Gln Leu Met Ala Pro	
610	615	620	
acc cca ccc ggc ctc agg aac	tcc ttg aac aga gca	agt ttc cga aag	1921
Thr Pro Pro Gly Leu Arg Asn	Ser Leu Asn Arg Ala	Ser Phe Arg Lys	
625	630	635	640
gca gac ctc tga gccacaagg	accaaagctg tacctagagg	aaccagcacc	1973
Ala Asp Leu			
cgggcctcag ctgtctgtgc	tgcgagggga gtctgccctg	gtgccactg ggctgtgggg	2033
tgaccacaact gtacttgggg	ctgggcctc tgccctgtg	tccccatctg tgtgcactga	2093
tgcttcctcc cttttttaat	ttaaaatggt ttttataagc	aaaaaaaaa aaaaaa	2149

<211> 643  
 <212> PRT  
 <213> Homo sapiens  
 <223> preliminary human CLASP-7 cDNA sequence

<400> 60

```

Leu Ser Glu Ala Arg Glu Ser Val Leu Gly Asp Leu Leu Lys Val Val
 1             5             10             15

Leu Tyr Ser Leu Gly Ser Ala Gln Ser Ala Leu Phe Leu Gln His Gly
      20             25             30

Leu Ala Thr Gln Arg Ala Leu Val Ser Lys Phe Pro Glu Leu Leu Phe
      35             40             45

Glu Glu Asp Thr Glu Leu Cys Ala Asp Leu Cys Leu Arg Leu Leu Arg
 50             55             60

His Cys Gly Ser Arg Ile Ser Thr Ile Arg Thr His Ala Ser Ala Ser
 65             70             75             80

Leu Tyr Leu Leu Met Arg Gln Asn Phe Glu Ile Gly His Asn Phe Ala
      85             90             95

Arg Val Lys Met Gln Val Thr Met Ser Leu Ser Ser Leu Val Gly Thr
      100            105            110

Thr Gln Asn Phe Ser Glu Glu His Leu Arg Arg Ser Leu Lys Thr Ile
      115            120            125

Leu Thr Tyr Ala Glu Glu Asp Met Gly Leu Arg Asp Ser Thr Phe Ala
      130            135            140

Glu Gln Val Gln Asp Leu Met Phe Asn Leu His Met Ile Leu Thr Asp
      145            150            155            160

Thr Val Lys Met Lys Glu His Gln Glu Asp Pro Glu Met Leu Ile Asp
      165            170            175

Leu Met Tyr Arg Ile Ala Arg Gly Tyr Gln Gly Ser Pro Asp Leu Arg
      180            185            190

Leu Thr Trp Leu Gln Asn Met Ala Gly Lys His Ala Glu Leu Gly Asn
      195            200            205

His Ala Glu Ala Ala Gln Cys Met Val His Ala Ala Ala Leu Val Ala
      210            215            220

Glu Tyr Leu Ala Leu Leu Glu Asp His Arg His Leu Pro Val Gly Cys
      225            230            235            240

Val Ser Phe Gln Asn Ile Ser Ser Asn Val Leu Glu Glu Ser Ala Ile
      245            250            255

Ser Asp Asp Ile Leu Ser Pro Asp Glu Glu Gly Phe Cys Ser Gly Lys
      260            265            270

His Phe Thr Glu Leu Gly Leu Val Gly Leu Leu Glu Gln Ala Ala Gly
      275            280            285

Tyr Phe Thr Met Gly Gly Leu Tyr Glu Ala Val Asn Glu Val Tyr Lys

```



290					295					300					
Asn	Leu	Ile	Pro	Ile	Leu	Glu	Ala	His	Arg	Asp	Tyr	Lys	Lys	Leu	Ala
305					310					315					320
Ala	Val	His	Gly	Lys	Leu	Gln	Glu	Ala	Phe	Thr	Lys	Ile	Met	His	Gln
				325					330					335	
Ser	Ser	Gly	Trp	Glu	Arg	Val	Phe	Gly	Thr	Tyr	Phe	Arg	Val	Gly	Phe
			340					345					350		
Tyr	Gly	Ala	His	Phe	Gly	Asp	Leu	Asp	Glu	Gln	Glu	Phe	Val	Tyr	Lys
		355					360					365			
Glu	Pro	Ser	Ile	Thr	Lys	Leu	Ala	Glu	Ile	Ser	His	Arg	Leu	Glu	Glu
		370					375					380			
Phe	Tyr	Thr	Glu	Arg	Phe	Gly	Asp	Asp	Val	Val	Glu	Ile	Ile	Lys	Asp
385					390					395					400
Ser	Tyr	Pro	Val	Asp	Lys	Ser	Lys	Leu	Asp	Ser	Gln	Lys	Ala	Tyr	Ile
				405					410					415	
Gln	Ile	Thr	Tyr	Val	Glu	Pro	Tyr	Phe	Asp	Thr	Tyr	Glu	Leu	Lys	Asp
			420					425					430		
Arg	Val	Thr	Tyr	Phe	Asp	Arg	Asn	Tyr	Gly	Leu	Arg	Thr	Phe	Leu	Phe
			435				440					445			
Cys	Thr	Pro	Phe	Thr	Pro	Asp	Gly	Arg	Ala	His	Gly	Glu	Leu	Pro	Glu
	450					455					460				
Gln	His	Lys	Arg	Lys	Thr	Leu	Leu	Ser	Thr	Asp	His	Ala	Phe	Pro	Tyr
465						470					475				480
Ile	Lys	Thr	Arg	Ile	Arg	Val	Cys	His	Arg	Glu	Glu	Thr	Val	Leu	Thr
				485					490					495	
Pro	Val	Glu	Val	Ala	Ile	Glu	Asp	Met	Gln	Lys	Lys	Thr	Arg	Glu	Leu
			500					505					510		
Ala	Phe	Ala	Thr	Glu	Gln	Asp	Pro	Pro	Asp	Ala	Lys	Met	Leu	Gln	Met
		515					520					525			
Val	Leu	Gln	Gly	Ser	Val	Gly	Pro	Thr	Val	Asn	Gln	Gly	Pro	Leu	Glu
	530					535					540				
Val	Ala	Gln	Val	Phe	Leu	Ala	Glu	Ile	Pro	Glu	Asp	Pro	Lys	Leu	Phe
545						550					555				560
Arg	His	His	Asn	Lys	Leu	Arg	Leu	Cys	Phe	Lys	Asp	Phe	Cys	Lys	Lys
				565					570					575	
Cys	Glu	Asp	Ala	Leu	Arg	Lys	Asn	Lys	Ala	Leu	Ile	Gly	Pro	Asp	Gln
			580					585					590		
Lys	Glu	Tyr	His	Arg	Glu	Leu	Glu	Arg	Asn	Tyr	Cys	Arg	Leu	Arg	Glu
		595					600					605			
Ala	Leu	Gln	Pro	Leu	Leu	Thr	Gln	Arg	Leu	Pro	Gln	Leu	Met	Ala	Pro
	610					615					620				

Thr Pro Pro Gly Leu Arg Asn Ser Leu Asn Arg Ala Ser Phe Arg Lys  
 625 630 635 640

Ala Asp Leu

<210> 61  
 <211> 120  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> exon 63800-63920

<400> 61  
 gcggggccgg ggccccgggc ggccggcgcg ggacgcgagg accatggctg cctccgagcg 60  
 ccgcgccttc gcgcacaaga tcaacaggta gtgtggccgc ggggccccct cccacctccc 120

<210> 62  
 <211> 141  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> exon 72530-72670

<400> 62  
 ccaatggccc cctccctatc tttccaggac ggtggccgca gaggtgcgga agcaggtgtc 60  
 ccgggaacgc agtggctccc cccactccag caggcgctgc agcagctccc tgggggtaag 120  
 tatttggggg gtccgcccc a 141

<210> 63  
 <211> 231  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> exon 73300-73530

<400> 63  
 tcacagccac tttgctccaa tccaggctccc actgactgaa gttgtcgagc ccctggactt 60  
 tgaggatgta cttctgagcc ggccaccaga tgctgagccc gggccccctca gggacctggt 120  
 agaattccca gctgatgact tggagctgct gctgcagccc cggaatgcc ggaccacgga 180  
 gcccgggatc cccaaggatg agtgggttca gcccacgcc ctctctgcct g 231

<210> 64  
 <211> 131  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> exon 73700-73830

<400> 64  
 gtctctgttt accctgatct tcttttgctg cagaaaactg gatgcccagg tgagggccgc 60  
 ggtggagatg tatattgagg actgggtcat tgtccacaga agtgagtct gacttagggg 120  
 cagctcaggg g 131

<210> 65  
 <211> 181  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> exon 74010-74190

<400> 65  
 cctgcccagc cccgttttct gctaggtatc agtacctgag tgcagcatac agccccgtca 60  
 ccacagacac acagcgggag cgacagaagg gcctcccccg ccaggctctt gagcaggatg 120  
 cttctggaga cgagaggtcc ggccctgagg actcgggtgag gaagccccctg gctgggggtca 180  
 c 181

<210> 66  
 <211> 281  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> exon 75170-75450

<400> 66  
 cagtgtttgc acattctcca ctggcagaat gactcccggc gtggctcggg ctccccggaa 60  
 gacacccctc gaagcagtgg tgcctctagc atcttcgacc tgaggaacct ggcagctgac 120  
 tcattgtctgc cctctctgct agagcgggag gccccagaag atgtggaccg gcgcaatgaa 180  
 acccttcgac ggcagcaccg gccccgggcc ctgctcacc cttaccgggc acctgacgag 240  
 gtgggtgccc cttcccagat atcagccaac cagcatttac t 281

<210> 67  
 <211> 151  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> exon 78100-78250

<400> 67  
 cccgcccagc tcccaccccc cactcttggc aggatgaagc cgtggaacgc tgtagccgcc 60  
 cagagccacc ccgcgagcac tttggacaaa ggatcttggc caagtgtctg tcgctcaagt 120  
 gagtatactg acatgtctct cttcttagat g 151

<210> 68  
 <211> 121  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> exon 80380-80500

<400> 68  
 cccctcctt cccatttact tgtaggttcg agattgaaat tgagcccatc tttgggatct 60  
 tggctctgta tgatgtgcgg gagaaaaaga aggtaggagg cccttttttc tctttcctcc 120  
 c 121

<210> 69  
 <211> 211  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> exon 80540-80750

<400> 69  
 gtggtggccc agctgcctct ggtgtcccca gatctcggag aacttctact tcgacctgaa 60  
 ctccgactcc atgaaggggc tgcttcgggc tcatggcacc caccctgccca tctccaccct 120  
 ggcccgtctt gccatcttct ctgtgacctt cccctcacct gacatcttcc tggatcatcaa 180  
 ggtgcctgct ggggctgggc aagggggtgg t 211

<210> 70  
 <211> 141  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> exon 82370-82510

<400> 70  
 gcctcactgg attcattcat ctgccccgca gttggagaag gtgcttcagc aaggggacat 60  
 cagtgagtgc tgtgagcctt acatgggtgtt gaaagaagtg gacacagcca aggtaagcgt 120  
 gtggaggctg gactaggggc a 141

<210> 71  
 <211> 221  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> exon 82540-82760

<400> 71  
 gctgagctgg cagggggacgg ggtctcccca cagaacaaag agaagctaga gaagctgcgc 60  
 ctggcgggccg agcagttctg caccgcctg ggccgctacc gcatgccctt cgctgggacg 120  
 gccgtgcact tggccaacat cgtgagcagc gctgggcagc tggaccggga ctctgactcg 180  
 gagggcggtg aggaggcggg gctaacaggc ttggggcggg g 221

<210> 72  
 <211> 201  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> exon 82860-83060

<400> 72  
 cttggtcccc cttttgtcat tgtcattccc tcccctagag cgccggccag cctggacaga 60  
 ccgccgccgt cggggggcccc aggaccgggc gagtagtggg gacgacgcct gcagtttctc 120  
 tggcttccgt ccagccacgc taactgtcac aaacttcttt aagcaggtgt cctaccctgg 180  
 ggccaggggac tctcccactc c 201

<210> 73  
 <211> 161

<212> DNA  
 <213> Homo sapiens

<220>  
 <223> exon 83100-83260

<400> 73  
 gccaggtg acgggagtgg gtcccatgta ggaggctgag cgactcagtg acgaggacct 60  
 cttcaagttc ctggctgaca tgaggcgccc gtcgtccctg ctgcggcgac tacgtcctgt 120  
 gactggtgcg tggcacaccc catacacaag aagtatcact c 161

<210> 74  
 <211> 221  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> exon 84050-84270

<400> 74  
 gtgcaaaccg gttcttccct tcccagccca gctcaagatc gacatttctc cggctcctga 60  
 aaatccccac ttctgcctct cccctgagct gcttcatatc aagccctacc cggaccccag 120  
 gggccggccc accaaggaga ttctggagtt ccccgcccgc gaagtctatg cccccatac 180  
 cagctacagg tacggcctct ggggcccagc tgggcacttg a 221

<210> 75  
 <211> 191  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> exon 87940-88130

<400> 75  
 gccctgtcc ctctgacacc cccatcctgc cccccacagg aacctgctgt acgtgtaccc 60  
 gcacagcctc aacttcagca gccgccaggg ctccgtgcgc aaccttgctg tgcgagtga 120  
 gtacatgaca ggcgaggacc ccagccaggg tctgccggtc agtggctgtg cccagggaa 180  
 ggggggtagg g 191

<210> 76  
 <211> 131  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> exon 88140-88270

<400> 76  
 tgggtccctc atgaatccac tctcccaggt catctttggc aagtccagct gcagtgaatt 60  
 taccgcgag gccttcacac cgggtggtcta ccataacaag tatgtagggg gacacgtgag 120  
 gaacttgagg g 131

<210> 77  
 <211> 211  
 <212> DNA  
 <213> Homo sapiens

&lt;220&gt;

&lt;223&gt; exon 88470-88680

&lt;400&gt; 77

```

gccccagca gatccccag cccgattctg ccaggtcccc cgagttctac gaggagtcca 60
agctgcatct tccagcctgc gtgacagaga accatcacct gctgttcacc ttctaccatg 120
tcagctgccca gccccggccg ggcactgccc tggagacacc cgtgggcttt actgtgagcc 180
gtccccctccc tccctccccc tgagccctcc t                                     211

```

&lt;210&gt; 78

&lt;211&gt; 191

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;223&gt; exon 88680-88870

&lt;400&gt; 78

```

tcgtcccccac acctggccgc agacctgacc tccagcctct cccagtgga tcccactgct 60
gcagcacggg cgctgagga cggcccccct ctgtctccca gtgtctgtgg accagccgcc 120
gcccagctat tccgtgctca caccgatgt atgtgccctg gagctcctgc ctgccaatgc 180
actgtcccca g                                     191

```

&lt;210&gt; 79

&lt;211&gt; 171

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;223&gt; exon 89360-89530

&lt;400&gt; 79

```

cagggagggc tgaccagtgc ccacctggtg cctccctccc acaggtggcg cttccgggca 60
tgcgctgggt ggacggtcac aaggcgctgt tcagtgtgga gtcacagcc gtgtcctctg 120
tgcaccccca ggtacggggt gggccgggaa ccaagagtcc cgccctgctc c       171

```

&lt;210&gt; 80

&lt;211&gt; 321

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;223&gt; exon 89660-89980

&lt;400&gt; 80

```

ttcattccct gaggccccac cctgctcact ccacatccct acccaggacc cctacctgga 60
caaattcttc accctgggtgc acgtcctgga ggaggagacc ttccattcc ggctcaagga 120
cactgtgctg agcgagggca acgtggagca ggagctgcgg gccagtcttg cagcactgcg 180
cctggccagc cccgaacccc ttgtggcctt ctcccaccac gtgctggaca agctcgtgcg 240
tctggtcatc aggcccccca tcatcagtgg ccagattggt aagcgaatgt ggcctcagac 300
ctcagtttcc ccatccacat g                                     321

```

&lt;210&gt; 81

&lt;211&gt; 251

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

<220>

<223> exon 90480-97030

<400> 81

```
agaggccttg ggccttgaa cttgacctct gctctgccct gcagtgaacc tgggccgtgg 60
agcctttgaa gcaatggccc atgtagtcag ccttggtcac cggagcctgg aggcagccca 120
ggatgcccgc ggtcactgcc cacagctggc tgcctacgct cactacgctt ttgccttcc 180
tggcactgag cccagcctcc cggatggtga gttttagtaa atccctgtga gacgagaaat 240
atctgggaga a 251
```

<210> 82

<211> 251

<212> DNA

<213> Homo sapiens

<220>

<223> exon 92870-93120

<400> 82

```
atcacatcag gtgggtgggt ggttgacctt attcactcca tcctcagggg cccctccagt 60
gacagtgcag gctgccacac tggcccgtgg ctctggtcgc cccgcaagcc tctacctggc 120
gcgttccaag agcatcagca gcagcaaccc tgacctcgcc gtggcccctg gctctgtgga 180
tgacgaggtt tcccgcattc tggccagcaa ggtagggcaa cggggggcct ggaatctcca 240
gcctcagtg t 251
```

<210> 83

<211> 181

<212> DNA

<213> Homo sapiens

<220>

<223> exon 97210-97390

<400> 83

```
ggcacctcgc actctgtgac ccctgcctct gtccccagct gcttcacgag gagctggctc 60
tgcatgggtt ggtcagcagc agtgccgtac gcgaggccat cctccagcac gcctgggtct 120
tcttccagct catggtgaga cccctcctc cctgcctggt ggcaagagac cccagtgga 180
g 181
```

<210> 84

<211> 221

<212> DNA

<213> Homo sapiens

<220>

<223> exon 98770-98990

<400> 84

```
caaatcccac ccacagccct ctcacccac cccaggtga agagtatggc gctgcacctg 60
ctgcttgccc agcgactaga cacacccgc aagctgcgct tccccggacg cttcctggac 120
gacatcactg ccttggtggg ctctgtgggc ctggagggtc tcacccgtgt ccacaagggt 180
agagatgcag ggtctcaatg tgggaagaaa cctgaggggag g 221
```

<210> 85

<211> 211

<212> DNA

<213> Homo sapiens

&lt;220&gt;

&lt;223&gt; exon 103130-103340

&lt;400&gt; 85

```

ggggctgagg tttgggtgtg tgggttgaca ggcacctgtg tccccaggat gtggagctgg 60
ccgagcacct caacgccagc ctggctttct tcctcagtga ctttctgtcc ctgggtggacc 120
ggggctttgt cttcagcctg gtccggggccc actacaagca ggtaggagtg ggcgtgggca 180
gggtgggcat ggcattggatg gaaggcggag c 211

```

&lt;210&gt; 86

&lt;211&gt; 251

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;223&gt; exon 103340-103590

&lt;400&gt; 86

```

caatgttgac atcactgatg gccacccttc tcctgcaggt ggccacgcgg ctccagtcgt 60
cccctaattcc agcagccctg ctgaccctgc gcattggaatt caccgcgcatc ctgtgcagcc 120
acgagcacta cgtgaccctc aacctccctt gctgccccct gtcacctcca gcctcgccct 180
ccccctctgt gtcctccacc acctcccagg tgggctgcct tcacttctgc ctctctctt 240
tgacctacaa c 251

```

&lt;210&gt; 87

&lt;211&gt; 231

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;223&gt; exon 103990-104220

&lt;400&gt; 87

```

tgacccttga ccgctggcat cccccatttt tccccactc tgcagagctc caccttctcc 60
agccaagccc cggaccccaa ggtgaccagc atgttcgaac tgagtggacc attccggcag 120
cagcacttcc tagctgggct cctgctgacg gagctggcac tggccctcga acctgaggct 180
gaaggggtgag cagagctcct gtctagcccc aggacagggtg ggacagtcca g 231

```

&lt;210&gt; 88

&lt;211&gt; 261

&lt;212&gt; DNA

&lt;213&gt; Homo sapiens

&lt;220&gt;

&lt;223&gt; exon 104220-104480

&lt;400&gt; 88

```

ggagccatgt ccaccctgtc ctgagcacct cattaccca tagggcattc ctgttgacac 60
agaaggccat cagtgtgtg cacagcctgc tatgtggcca tgacctgac ccccgctacg 120
ccgaggccac tgtgaaggct cgtgtggccg agctgtacct gccactgcta tcgattgcac 180
gggatacctt gccacggctg catgactttg ctggtcagtg ggccagggga agatggggtc 240
acatgatcca gggacttggt c 261

```

&lt;210&gt; 89

&lt;211&gt; 251

&lt;212&gt; DNA



<213> Homo sapiens

<220>

<223> exon 108850-109100

<400> 89

```

accaagggtt tatctttctt tccctctgtc tttccctgcc agaggggcca ggtcagcggg 60
caagactggc ctcaatgctt gactcagaca cagaaggcga aggggacatt gcgggtacca 120
tcaacccctc tgtggccatg gccattgctg gtggcccccct agcccctggc tcccggggcca 180
gcatctccca gggggcacca acggtgagta gggaggcttg tccccataga catcatccac 240
tttgaatgag a 251

```

<210> 90

<211> 271

<212> DNA

<213> Homo sapiens

<220>

<223> exon 109140-109410

<400> 90

```

tcacatggag aaaatggaaa ttgactttga ttctctctg gccccaggct tctcgcgcag 60
gctgtgccct ctctgctgag tcaagccgga ccttgctggc gtgtgtgctg tgggtgctga 120
aaaacaccga gccggcgctc ctgcagcgtt gggccactga cctgacactc ccccagctgg 180
gacgtctgtt ggatttctg tacctttgcc tagctgcctt tgagtacaag gtttgagggc 240
gtgggcagga gatgatggag gaggcaggct a 271

```

<210> 91

<211> 221

<212> DNA

<213> Homo sapiens

<220>

<223> exon 110310-110530

<400> 91

```

gaaaagagca gagtcagcct ggaaccccag ttctctgcac ccccagggga aaaaggcctt 60
tgaacgcata aacagcctca cattcaaaaa atctctggat atgaaggcgc ggctagagga 120
agccattctg ggtaccatcg gagctcgaca agaaatgggt cggcgaagtc gtggaagag 180
ggtgacatac ccacgtgtcc ccatcccacc agctgctccc a 221

```

<210> 92

<211> 171

<212> DNA

<213> Homo sapiens

<220>

<223> exon 110770-110940

<400> 92

```

tgtgttttta cgcattctgt atcgtgcacc caccgcgtctc agagaggagc ccgtttggga 60
atccggagaa tgtgcgctgg cggaagagcg tcacacactg gaagcaaaac tcagaccgcg 120
tggacaagta ggtgtgggca ggagggtgtc tgctgagttc agaacagttt g 171

```

<210> 93

<211> 181

<212> DNA

<213> Homo sapiens

<220>

<223> exon qqg590-111770

<400> 93

```
atctcacccc gagtggggccc ccaagacctc ctttcccctt ccaggaccaa ggatgaaatg 60
gaacacgagg ccttggtgga agggaaacctg gcaaccgagg caagcctagt gggtctggac 120
acactggaga tcatcgtgca ggtagggctt gatccagcat ctgccttgtg ctctgagccc 180
a                                                    181
```

<210> 94

<211> 221

<212> DNA

<213> Homo sapiens

<220>

<223> exon 111830-112050

<400> 94

```
accctaggct ctaacacctg gatttctgac ccccttcctt ccagacgggtg atgctttcag 60
aagcccggga gagcgtcttg ggggcagtgc tgaagggtgt gctgtacagc ctgggcagtg 120
cccagagtgc cctcttcttg cagcatggcc tggccaccca gagggccctt gtgtccaagg 180
tgagcaccac tcaacaacca tgattcttag aaaaacagta g                                                    221
```

<210> 95

<211> 241

<212> DNA

<213> Homo sapiens

<220>

<223> exon 112910-113140

<400> 95

```
aacggggagg ggctggacag tgtctgtctg ggtccttggg ggcagttccc ggagctgctg 60
ttcgaggagg acacggagct gtgtgccgac ctgtgcctga ggctcctacg acactgtggc 120
agccgcatca gcaccatccg cagcgacgcc agcgctcgc tgtacctgct catgcgacag 180
aacttcgaga tcggccacgt gagtgggggc taggaggcat ggtccacaca tggctctggt 240
c                                                    241
```

<210> 96

<211> 251

<212> DNA

<213> Homo sapiens

<220>

<223> exon 114090-114340

<400> 96

```
tctgagactc ccggctccac cctcccggcc ctgtccctgc agaactttgc ccgtgtgaag 60
atgcaggta ccatgtctct ctgcctcctg gtggggacga cgcagaactt cagtgaagag 120
cacctgcgac gttcactcaa aaccatcctc acctatgctg aggaggacat ggggctgcgg 180
gacagcacct tcgcagagca ggtgacacct gctgggtccc cgccccgcct ccccttcata 240
taactcccaa c                                                    251
```

<210> 97

<211> 181

<212> DNA  
 <213> Homo sapiens

<220>  
 <223> exon 114370-114550

<400> 97  
 atgctctcat tggcccctgg acgttccccg gctccaggtc caggacctga tgttcaacct 60  
 gcacatgata ctgacggaca cgggtgaagat gaaggaacac caggaggacc ctgagatgct 120  
 catcgacctc atgtacaggt gaggtggggc agctggcacc ttcagccacg cccacgcccc 180  
 a 181

<210> 98  
 <211> 271  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> exon 116900-117170

<400> 98  
 aggtgagtcc cctcctcaca tccccctca cctggactcc agaattgccc ggggctacca 60  
 gggctcaccg gaccttcggc tgacctgggt gcagaacatg gccgggaagc acgcggacgt 120  
 gggcaaccac gccgaggccg cccagtgcac ggtgcacgcg gccgccctcg tggctgagta 180  
 cctcgccctg ctcgaggacc agcgccacct gcccgtggct ggcgatttcc ttccagggtga 240  
 gtggccaggg gttggcaggt ggcggacggc a 271

<210> 99  
 <211> 241  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> exon 117170-117410

<400> 99  
 acgagtgcag tggggaccag ggtctgacgc cacctctccc accccagaac atctcatcca 60  
 acgtgctaga ggagtccgcc atctccgacg acatcctgtc gcccgacgag gagggttct 120  
 gctccgggaa gcacttcact gagctggggc tggtaggggt gctggaacag gcagccggct 180  
 acttcaccat ggtgaggcct tggggactgg gtgcaggaga gggggctcgg gccagggagg 240  
 t 241

<210> 100  
 <211> 229  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> exon 121670-121900

<400> 100  
 gagaggaaga cagtttgggg aatcctgacc ccacctcacc ctcagggcgg gctctacgag 60  
 gcggtgaatg aggtctacaa gaacctcatc cccatcctgg aagccaccg tgactacaag 120  
 aagctggccg cgggtgcacg caaactgcag gaggccttca ccaagatcat gcaccagggtg 180  
 ggcccaggac cccctcccca gacccaccc tcagcccccac tctcatcc 229

<210> 101

<211> 91  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> exon 121910-122000

<400> 101  
 ccccagggat ctgctgacct tgacccttct cttccccaca gagttccggc tgggaggtga 60  
 gtcagccttg gtggacagcc acctgcctct g 91

<210> 102  
 <211> 221  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> exon 123290-123510

<400> 102  
 tccagcaggg gcctcccgga caaccacacc ctttctcaca gccccagcgc gtgttcggga 60  
 cgtatttccg cgtgggcttc tacggcgccc acttcgggtga cctggatgag caggagtttg 120  
 tgtacaagga gccatcgatc acgaagctgg cagagatctc acaccggctg gaggcattgc 180  
 cttgtgggtg ggggtggaac ggggcatggg gctgccttgg g 221

<210> 103  
 <211> 124  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> exon 123510-123633 (end clone)

<400> 103  
 ggctggagta ggggctgtcc ctgggtggcc ccgagtcagc cctgtgtctc caggagttct 60  
 acacggagag atttggcgac gacgtcggtg agattatcaa agactctaac cctgtggaca 120  
 agtc 124

<210> 104  
 <211> 1951  
 <212> DNA  
 <213> Homo sapiens

<220>  
 <223> putative human CLASP-7 promoter region

<400> 104  
 gggcatgtgg ctcatctctg taatcccggc actttgggag gccgaggcgg gtggatcacc 60  
 tgaggtcagg agctccagac cagcctggcc aacatgggtga aaccccgctct ctactaaaaa 120  
 tacaaaaaat tagccagggtg tgatgggtggg tgccgtgtaat cccagctact cgggagggtg 180  
 aggcaggaga atcgcttgaa cctgggaggc agagggtgcg gtgagccgag attgtgccat 240  
 tgcactccag tctggggcaac aagagcgaaa tgccacctca aaataaataa ataaataaat 300  
 aaataaataa ataaataaat aaataaataa tagaggataa aatgccagca acccatagat 360  
 gggaatgaga acagcacgtg caaaggccct gaggcagagc cacggccttg tctgattcaa 420  
 cctcaaattc tccctggggc atttgctgac cagggaaaga agggctgtcc aggaggaagg 480  
 acctgccggt gcagaggcat gcagggtgaga aaggggtgag ctctccaga ggggagtggtc 540  
 ggctggagaa ttctctaaaa atgctgcagc agtgctggga gagaggccag tggggagaga 600  
 tttgagacca tagattaacc aagacatccc cacctcttcc tcttggtaga ggcggccccc 660

```

aaagtctaga ctcccaaact ggctcactca ggtcccacca cctggacctg gggcacatct 720
ccgagcactc cagtgcctag ccaggctcct ctgactccca tgctgtagac tgggagcacg 780
gacaatgcag gcgctggaga cccctgtgag tcacactgag caagcaccg aacacctctg 840
tgcctcagtt tactcatctg taaaaggagg aaaacaataa tttcttctgc atgtgtgaat 900
tgcagggccca ggctcaatga catcttagca attagacttt ttgagacagg gtctcgtctc 960
gtcaccacagg ctggattgaa atggcacaaat cacagctcac tgcagccttg acctcccagg 1020
ctcaagcgat cctcctccct cagactccca agtagctgag attacaggca cacaccacca 1080
tgcctgggta atttttgcat tttttgtgga cacgggggtct cattatgttg cccagggttg 1140
tctccaactc ctggggtcaa acaatcctcc tgcttggcc cccacagtg ctgggattac 1200
aggcatgagc caccatgcac ggccacgatt ataactacag gtatgattat tagatacatg 1260
aacatcgtaa ttgttttcca gccaggagtc agagggcaga aagagcgccc cccaaacccc 1320
ggaaatctgg ggcctaccca gcctgggtcc cagcgctcc cctccctccc tccctcctga 1380
gcttcagttt cccagccct gctcctgggg tggtaaagacc accccactaa accccgggag 1440
cctgggggtcc acctagccc ggtctcagcg cctcccttcc cctccctccc cctcaggctc 1500
agtcttctca gccagctcc cagggtggaa agagcgcccc cgccagctcg ggagtctggg 1560
gcacccccag tctgggtccc agcgctcct ctccctaact tccctcctca gcctcagttt 1620
ccccagccct tctcctaggg tagaaagagc gtccccccag cccgggagtc tggggcccg 1680
ccagcctgga tcccggggcc tcctctccgt cccagcctc agtttcccca gccccagga 1740
ctccaggcga cccctccggc ctgcaggggc agcacggagc ggcccgggcc acccggaagg 1800
gccccgcccc cgcgccggcc ccgccccgcc ccggtgccc agaaccggga ggcgcgcgcg 1860
gcggcgggggc cgggggcccg ggcgcgcgcg gcgggacgcg aggaccatgg ctgcctccga 1920
gcgcccgcgcc ttcgcgcaca agatcaacag g 1951

```

<210> 105

<211> 2008

<212> PRT

<213> Homo sapiens

<220>

<223> human CLASP-4

<400> 105

```

Met Phe Pro Met Glu Asp Ile Ser Ile Ser Val Ile Gly Arg Gln Arg
 1             5             10             15

Arg Thr Val Gln Ser Thr Val Pro Glu Asp Ala Glu Lys Arg Ala Gln
      20             25             30

Ser Leu Phe Val Lys Glu Cys Ile Lys Thr Tyr Ser Thr Asp Trp His
      35             40             45

Val Val Asn Tyr Lys Tyr Glu Asp Phe Ser Gly Asp Phe Arg Met Leu
      50             55             60

Pro Cys Lys Ser Leu Arg Pro Glu Lys Ile Pro Asn His Val Phe Glu
      65             70             75             80

Ile Asp Glu Asp Cys Glu Lys Asp Glu Asp Ser Ser Ser Leu Cys Ser
      85             90             95

Gln Lys Gly Gly Val Ile Lys Gln Gly Trp Leu His Lys Ala Asn Val
      100            105            110

Asn Ser Thr Ile Thr Val Thr Met Lys Val Phe Lys Arg Arg Tyr Phe
      115            120            125

Tyr Leu Thr Gln Leu Pro Asp Gly Ser Tyr Ile Leu Asn Ser Tyr Lys
      130            135            140

Asp Glu Lys Asn Ser Lys Glu Ser Lys Gly Cys Ile Tyr Leu Asp Ala

```

145		150		155		160
Cys Ile Asp Val Val Gln Cys Pro Lys Met Arg Arg His Ala Phe Glu						
		165		170		175
Leu Lys Met Leu Asp Lys Tyr Ser His Tyr Leu Ala Ala Glu Thr Glu						
		180		185		190
Gln Glu Met Glu Glu Trp Leu Ile Thr Leu Lys Lys Ile Ile Gln Ile						
		195		200		205
Asn Thr Asp Ser Leu Val Gln Glu Lys Lys Glu Thr Val Glu Thr Ala						
		210		215		220
Gln Asp Asp Glu Thr Ser Ser Gln Gly Lys Ala Glu Asn Ile Met Ala						
		225		230		235
Ser Leu Glu Arg Ser Met His Pro Glu Leu Met Lys Tyr Gly Arg Glu						
		245		250		255
Thr Glu Gln Leu Asn Lys Leu Ser Arg Gly Asp Gly Arg Gln Asn Leu						
		260		265		270
Phe Ser Phe Asp Ser Glu Val Gln Arg Leu Asp Phe Ser Gly Ile Glu						
		275		280		285
Pro Asp Ile Lys Pro Phe Glu Glu Lys Cys Asn Lys Arg Phe Leu Val						
		290		295		300
Asn Cys His Asp Leu Thr Phe Asn Ile Leu Gly Gln Ile Gly Asp Asn						
		305		310		315
Ala Lys Gly Pro Pro Thr Asn Val Glu Pro Phe Phe Ile Asn Leu Ala						
		325		330		335
Leu Phe Asp Val Lys Asn Asn Cys Lys Ile Ser Ala Asp Phe His Val						
		340		345		350
Asp Leu Asn Pro Pro Ser Val Arg Glu Met Leu Trp Gly Ser Ser Thr						
		355		360		365
Gln Leu Ala Ser Asp Gly Ser Pro Lys Gly Ser Ser Pro Glu Ser Tyr						
		370		375		380
Ile His Gly Ile Ala Glu Ser Gln Leu Arg Tyr Ile Gln Gln Gly Ile						
		385		390		395
Phe Ser Val Thr Asn Pro His Pro Glu Ile Phe Leu Val Ala Arg Ile						
		405		410		415
Glu Lys Val Leu Gln Gly Asn Ile Thr His Cys Ala Glu Pro Tyr Ile						
		420		425		430
Lys Asn Ser Asp Pro Val Lys Thr Ala Gln Lys Val His Arg Thr Ala						
		435		440		445
Lys Gln Val Cys Ser Arg Leu Gly Gln Tyr Arg Met Pro Phe Ala Trp						
		450		455		460
Ala Ala Arg Pro Ile Phe Lys Asp Thr Gln Gly Ser Leu Asp Leu Asp						
		465		470		475
						480

Gly	Arg	Phe	Ser	Pro	Leu	Tyr	Lys	Gln	Asp	Ser	Ser	Lys	Leu	Ser	Ser		
				485					490					495			
Glu	Asp	Ile	Leu	Lys	Leu	Leu	Ser	Glu	Tyr	Lys	Lys	Pro	Glu	Lys	Thr		
			500					505					510				
Lys	Leu	Gln	Ile	Ile	Pro	Gly	Gln	Leu	Asn	Ile	Thr	Val	Glu	Cys	Val		
		515					520					525					
Pro	Val	Asp	Leu	Ser	Asn	Cys	Ile	Thr	Ser	Ser	Tyr	Val	Pro	Leu	Lys		
	530					535					540						
Pro	Phe	Glu	Lys	Asn	Cys	Gln	Asn	Ile	Thr	Val	Glu	Val	Glu	Glu	Phe		
545					550					555					560		
Val	Pro	Glu	Met	Thr	Lys	Tyr	Cys	Tyr	Pro	Phe	Thr	Ile	Tyr	Lys	Asn		
			565						570					575			
His	Leu	Tyr	Val	Tyr	Pro	Leu	Gln	Leu	Lys	Tyr	Asp	Ser	Gln	Lys	Thr		
			580					585					590				
Phe	Ala	Lys	Ala	Arg	Asn	Ile	Ala	Val	Cys	Val	Glu	Phe	Arg	Asp	Ser		
		595					600					605					
Asp	Glu	Ser	Asp	Ala	Ser	Ala	Leu	Lys	Cys	Ile	Tyr	Gly	Lys	Pro	Ala		
	610					615					620						
Gly	Ser	Val	Phe	Thr	Thr	Asn	Ala	Tyr	Ala	Val	Val	Ser	His	His	Asn		
625					630					635					640		
Gln	Asn	Pro	Glu	Phe	Tyr	Asp	Glu	Ile	Lys	Ile	Glu	Leu	Pro	Ile	His		
			645						650					655			
Leu	His	Gln	Lys	His	His	Leu	Leu	Phe	Thr	Phe	Tyr	His	Val	Ser	Cys		
			660					665					670				
Glu	Ile	Asn	Thr	Lys	Gly	Thr	Thr	Lys	Lys	Gln	Asp	Thr	Val	Glu	Thr		
	675						680					685					
Pro	Val	Gly	Phe	Ala	Trp	Val	Pro	Leu	Leu	Lys	Asp	Gly	Arg	Ile	Ile		
	690					695					700						
Thr	Phe	Glu	Gln	Gln	Leu	Pro	Val	Ser	Ala	Asn	Leu	Pro	Pro	Gly	Tyr		
705					710					715				720			
Leu	Asn	Leu	Asn	Asp	Ala	Glu	Ser	Arg	Arg	Gln	Cys	Asn	Val	Asp	Ile		
			725					730						735			
Lys	Trp	Val	Asp	Gly	Ala	Lys	Pro	Leu	Leu	Lys	Phe	Lys	Ser	His	Leu		
		740						745					750				
Glu	Ser	Thr	Ile	Tyr	Thr	Gln	Asp	Leu	His	Val	His	Lys	Phe	Phe	His		
		755					760					765					
His	Cys	Gln	Leu	Ile	Gln	Ser	Gly	Ser	Lys	Glu	Val	Pro	Gly	Glu	Leu		
	770					775					780						
Ile	Lys	Tyr	Leu	Lys	Cys	Leu	His	Ala	Met	Glu	Ile	Gln	Val	Met	Ile		
785					790					795					800		

Gln Phe Leu Pro Val Ile Leu Met Gln Leu Phe Arg Val Leu Thr Asn  
 805 810 815  
 Met Thr His Glu Asp Asp Val Pro Ile Asn Cys Thr Met Val Leu Leu  
 820 825 830  
 His Ile Val Ser Lys Cys His Glu Glu Gly Leu Asp Ser Tyr Leu Arg  
 835 840 845  
 Ser Phe Ile Lys Tyr Ser Phe Arg Pro Glu Lys Pro Ser Ala Pro Gln  
 850 855 860  
 Ala Gln Leu Ile His Glu Thr Leu Ala Thr Thr Met Ile Ala Ile Leu  
 865 870 875 880  
 Lys Gln Ser Ala Asp Phe Leu Ser Ile Asn Lys Leu Leu Lys Tyr Ser  
 885 890 895  
 Trp Phe Phe Phe Glu Ile Ile Ala Lys Ser Met Ala Thr Tyr Leu Leu  
 900 905 910  
 Glu Glu Asn Lys Ile Lys Leu Pro Arg Gly Gln Arg Phe Pro Glu Thr  
 915 920 925  
 Tyr His His Val Leu His Ser Leu Leu Leu Ala Ile Ile Pro His Val  
 930 935 940  
 Thr Ile Arg Tyr Ala Glu Ile Pro Asp Glu Ser Arg Asn Val Asn Tyr  
 945 950 955 960  
 Ser Leu Ala Ser Phe Leu Lys Arg Cys Leu Thr Leu Met Asp Arg Gly  
 965 970 975  
 Phe Ile Phe Asn Leu Ile Asn Asp Tyr Ile Ser Gly Phe Ser Pro Lys  
 980 985 990  
 Asp Pro Lys Val Leu Ala Glu Tyr Lys Phe Glu Phe Leu Gln Thr Ile  
 995 1000 1005  
 Cys Asn His Glu His Tyr Ile Pro Leu Asn Leu Pro Met Ala Phe Ala  
 1010 1015 1020  
 Lys Pro Lys Leu Gln Arg Val Gln Asp Ser Asn Leu Glu Tyr Ser Leu  
 1025 1030 1035 1040  
 Ser Asp Glu Tyr Cys Lys His His Phe Leu Val Gly Leu Leu Leu Arg  
 1045 1050 1055  
 Glu Thr Ser Ile Ala Leu Gln Asp Asn Tyr Glu Ile Arg Tyr Thr Ala  
 1060 1065 1070  
 Ile Ser Val Ile Lys Asn Leu Leu Ile Lys His Ala Phe Asp Thr Arg  
 1075 1080 1085  
 Tyr Gln His Lys Asn Gln Gln Ala Lys Ile Ala Gln Leu Tyr Leu Pro  
 1090 1095 1100  
 Phe Val Gly Leu Leu Leu Glu Asn Ile Gln Arg Leu Ala Gly Arg Asp  
 1105 1110 1115 1120  
 Thr Leu Tyr Ser Cys Ala Ala Met Pro Asn Ser Ala Ser Arg Asp Glu



1125	1130	1135
Phe Pro Cys Gly Phe Thr Ser Pro Ala Asn Arg Gly Ser Leu Ser Thr 1140	1145	1150
Asp Lys Asp Thr Ala Tyr Gly Ser Phe Gln Asn Gly His Gly Ile Lys 1155	1160	1165
Arg Glu Asp Ser Arg Gly Ser Leu Ile Pro Glu Gly Ala Thr Gly Phe 1170	1175	1180
Pro Asp Gln Gly Asn Thr Gly Glu Asn Thr Arg Gln Ser Ser Thr Arg 1185	1190	1195
Ser Ser Val Ser Gln Tyr Asn Arg Leu Asp Gln Tyr Glu Ile Arg Ser 1205	1210	1215
Leu Leu Met Cys Tyr Leu Tyr Ile Val Lys Met Ile Ser Glu Asp Thr 1220	1225	1230
Leu Leu Thr Tyr Trp Asn Lys Val Ser Pro Gln Glu Leu Ile Asn Ile 1235	1240	1245
Leu Ile Leu Leu Glu Val Cys Leu Phe His Phe Arg Tyr Met Gly Lys 1250	1255	1260
Arg Asn Ile Ala Arg Val His Asp Ala Trp Leu Ser Lys His Phe Gly 1265	1270	1275
Ile Asp Arg Lys Ser Gln Thr Met Pro Ala Leu Arg Asn Arg Ser Gly 1285	1290	1295
Val Met Gln Ala Arg Leu Gln His Leu Ser Ser Leu Glu Ser Ser Phe 1300	1305	1310
Thr Leu Asn His Ser Ser Thr Thr Thr Glu Ala Asp Ile Phe His Gln 1315	1320	1325
Ala Leu Leu Glu Gly Asn Thr Ala Thr Glu Val Ser Leu Thr Val Leu 1330	1335	1340
Asp Thr Ile Ser Phe Phe Thr Gln Cys Phe Lys Thr Gln Leu Leu Asn 1345	1350	1355
Asn Asp Gly His Asn Pro Leu Met Lys Lys Val Phe Asp Ile His Leu 1365	1370	1375
Ala Phe Leu Lys Asn Gly Gln Ser Glu Val Ser Leu Lys His Val Phe 1380	1385	1390
Ala Ser Leu Arg Ala Phe Ile Ser Lys Phe Pro Ser Ala Phe Phe Lys 1395	1400	1405
Gly Arg Val Asn Met Cys Ala Ala Phe Cys Tyr Glu Val Leu Lys Cys 1410	1415	1420
Cys Thr Ser Lys Ile Ser Ser Thr Arg Asn Glu Ala Ser Ala Leu Leu 1425	1430	1435
Tyr Leu Leu Met Arg Asn Asn Phe Glu Tyr Thr Lys Arg Lys Thr Phe 1445	1450	1455

Leu Arg Thr His Leu Gln Ile Ile Ile Ala Val Ser Gln Leu Ile Ala  
 1460 1465 1470  
 Asp Val Ala Leu Ser Gly Gly Ser Arg Phe Gln Glu Ser Leu Phe Ile  
 1475 1480 1485  
 Ile Asn Asn Phe Ala Asn Ser Asp Arg Pro Met Lys Ala Thr Ala Phe  
 1490 1495 1500  
 Pro Ala Glu Val Lys Asp Leu Thr Lys Arg Ile Arg Thr Val Leu Met  
 1505 1510 1515 1520  
 Ala Thr Ala Gln Met Lys Glu His Glu Lys Asp Pro Glu Met Leu Ile  
 1525 1530 1535  
 Asp Leu Gln Tyr Ser Leu Ala Lys Ser Tyr Ala Ser Thr Pro Glu Leu  
 1540 1545 1550  
 Arg Lys Thr Trp Leu Asp Ser Met Ala Lys Ile His Val Lys Asn Gly  
 1555 1560 1565  
 Asp Phe Ser Glu Ala Ala Met Cys Tyr Val His Val Ala Ala Leu Val  
 1570 1575 1580  
 Ala Glu Phe Leu His Arg Lys Lys Leu Phe Pro Asn Gly Cys Ser Ala  
 1585 1590 1595 1600  
 Phe Lys Lys Ile Thr Pro Asn Ile Asp Glu Glu Gly Ala Met Lys Glu  
 1605 1610 1615  
 Asp Ala Gly Met Met Asp Val His Tyr Ser Glu Glu Val Leu Leu Glu  
 1620 1625 1630  
 Leu Leu Glu Gln Cys Val Asp Gly Leu Trp Lys Ala Glu Arg Tyr Glu  
 1635 1640 1645  
 Ile Ile Ser Glu Ile Ser Lys Leu Ile Val Pro Ile Tyr Glu Lys Arg  
 1650 1655 1660  
 Arg Glu Phe Glu Lys Leu Thr Gln Val Tyr Arg Thr Leu His Gly Ala  
 1665 1670 1675 1680  
 Tyr Thr Lys Ile Leu Glu Val Met His Thr Lys Lys Arg Leu Leu Gly  
 1685 1690 1695  
 Thr Phe Phe Arg Val Ala Phe Tyr Gly Gln Ser Phe Phe Glu Glu Glu  
 1700 1705 1710  
 Asp Gly Lys Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr Gly Leu Ser  
 1715 1720 1725  
 Glu Ile Ser Leu Arg Leu Val Lys Leu Tyr Gly Glu Lys Phe Gly Thr  
 1730 1735 1740  
 Glu Asn Val Lys Ile Ile Gln Asp Ser Asp Lys Val Asn Ala Lys Glu  
 1745 1750 1755 1760  
 Leu Asp Pro Lys Tyr Ala His Ile Gln Val Thr Tyr Val Lys Pro Tyr  
 1765 1770 1775

Phe Asp Asp Lys Glu Leu Thr Glu Arg Lys Thr Glu Phe Glu Arg Asn  
 1780 1785 1790  
 His Asn Ile Ser Arg Phe Val Phe Glu Ala Pro Tyr Thr Leu Ser Gly  
 1795 1800 1805  
 Lys Lys Gln Gly Cys Ile Glu Glu Gln Cys Lys Arg Arg Thr Ile Leu  
 1810 1815 1820  
 Thr Thr Ser Asn Ser Phe Pro Tyr Val Lys Lys Arg Ile Pro Ile Asn  
 1825 1830 1835 1840  
 Cys Glu Gln Gln Ile Asn Leu Lys Pro Ile Asp Gly Ala Thr Asp Glu  
 1845 1850 1855  
 Ile Lys Asp Lys Thr Ala Glu Leu Gln Lys Leu Cys Ser Ser Thr Asp  
 1860 1865 1870  
 Val Asp Met Ile Gln Leu Gln Leu Lys Leu Gln Gly Trp Val Ser Val  
 1875 1880 1885  
 Gln Val Asn Ala Gly Pro Leu Ala Tyr Ala Arg Ala Phe Leu Asn Asp  
 1890 1895 1900  
 Ser Gln Ala Ser Lys Tyr Pro Pro Lys Lys Val Ser Glu Leu Lys Asp  
 1905 1910 1915 1920  
 Met Phe Arg Lys Phe Ile Gln Ala Cys Ser Ile Ala Leu Glu Leu Asn  
 1925 1930 1935  
 Glu Arg Leu Ile Lys Glu Asp Gln Val Glu Tyr His Glu Gly Leu Lys  
 1940 1945 1950  
 Ser Asn Phe Arg Asp Met Val Lys Glu Leu Ser Asp Ile Ile His Glu  
 1955 1960 1965  
 Gln Ile Leu Gln Glu Asp Thr Met His Ser Pro Trp Met Ser Asn Thr  
 1970 1975 1980  
 Leu His Val Phe Cys Ala Ile Ser Gly Thr Ser Ser Asp Arg Gly Tyr  
 1985 1990 1995 2000  
 Gly Ser Pro Arg Tyr Ala Glu Val  
 2005

<210> 106  
 <211> 2015  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <223> human CLASP-5

<400> 106  
 Met Thr His Leu Asn Ser Leu Asp Val Gln Leu Ala Gln Glu Leu Gly  
 1 5 10 15  
 Asp Phe Thr Asp Asp Asp Leu Asp Val Val Phe Thr Pro Lys Glu Cys  
 20 25 30

Arg Thr Leu Gln Pro Ser Leu Pro Glu Glu Gly Val Glu Leu Asp Pro  
           35                          40                          45  
 His Val Arg Asp Cys Val Gln Thr Tyr Ile Arg Glu Trp Leu Ile Val  
           50                          55                          60  
 Asn Arg Lys Asn Gln Gly Ser Pro Glu Ile Cys Gly Phe Lys Lys Thr  
           65                          70                          75                          80  
 Gly Ser Arg Lys Asp Phe His Lys Thr Leu Pro Lys Gln Thr Phe Glu  
                           85                          90                          95  
 Ser Glu Thr Leu Glu Cys Ser Glu Pro Ala Ala Gln Ala Gly Pro Arg  
                           100                          105                          110  
 His Leu Asn Val Leu Cys Asp Val Ser Gly Lys Gly Pro Val Thr Ala  
           115                          120                          125  
 Cys Asp Phe Asp Leu Arg Ser Leu Gln Pro Asp Lys Arg Leu Glu Asn  
           130                          135                          140  
 Leu Leu Gln Gln Val Ser Ala Glu Asp Phe Glu Lys Gln Asn Glu Glu  
           145                          150                          155                          160  
 Ala Arg Arg Thr Asn Arg Gln Ala Glu Leu Phe Ala Leu Tyr Pro Ser  
                           165                          170                          175  
 Val Asp Glu Glu Asp Ala Val Glu Ile Arg Pro Val Pro Glu Cys Pro  
           180                          185                          190  
 Lys Glu His Leu Gly Asn Arg Ile Leu Val Lys Leu Leu Thr Leu Lys  
           195                          200                          205  
 Phe Glu Ile Glu Ile Glu Pro Leu Phe Ala Ser Ile Ala Leu Tyr Asp  
           210                          215                          220  
 Val Lys Glu Arg Lys Lys Ile Ser Glu Asn Phe His Cys Asp Leu Asn  
           225                          230                          235                          240  
 Ser Asp Gln Phe Lys Gly Phe Leu Arg Ala His Thr Pro Ser Val Ala  
                           245                          250                          255  
 Ala Ser Ser Gln Ala Arg Ser Ala Val Phe Ser Val Thr Tyr Pro Ser  
                           260                          265                          270  
 Ser Asp Ile Tyr Leu Val Val Lys Ile Glu Lys Val Leu Gln Gln Gly  
           275                          280                          285  
 Asp Ile Gly Asp Cys Ala Glu Pro Tyr Thr Val Ile Lys Glu Ser Asp  
           290                          295                          300  
 Gly Gly Lys Ser Lys Glu Lys Ile Glu Lys Leu Lys Leu Gln Ala Glu  
           305                          310                          315                          320  
 Ser Phe Cys Gln Arg Leu Gly Lys Tyr Arg Met Pro Phe Ala Trp Ala  
                           325                          330                          335  
 Pro Ile Ser Leu Ser Ser Phe Phe Asn Val Ser Thr Leu Glu Arg Glu  
                           340                          345                          350  
 Val Thr Asp Val Asp Ser Val Val Gly Arg Ser Pro Val Gly Glu Arg

355					360					365					
Arg	Thr	Leu	Ala	Gln	Ser	Arg	Arg	Leu	Ser	Glu	Arg	Ala	Leu	Ser	Leu
	370					375					380				
Glu	Glu	Asn	Gly	Val	Gly	Ser	Asn	Phe	Lys	Thr	Ser	Thr	Leu	Ser	Val
385					390					395					400
Ser	Ser	Phe	Phe	Lys	Gln	Glu	Gly	Asp	Arg	Leu	Ser	Asp	Glu	Asp	Leu
				405					410					415	
Phe	Lys	Phe	Leu	Ala	Asp	Tyr	Lys	Arg	Ser	Ser	Ser	Leu	Gln	Arg	Arg
			420					425					430		
Val	Lys	Ser	Ile	Pro	Gly	Leu	Leu	Arg	Leu	Glu	Ile	Ser	Thr	Ala	Pro
			435				440					445			
Glu	Ile	Ile	Asn	Cys	Cys	Leu	Thr	Pro	Glu	Met	Leu	Pro	Val	Lys	Pro
	450					455					460				
Phe	Pro	Glu	Asn	Arg	Thr	Arg	Pro	His	Lys	Glu	Ile	Leu	Glu	Phe	Pro
465					470					475					480
Thr	Arg	Glu	Val	Tyr	Val	Pro	His	Thr	Val	Tyr	Arg	Asn	Leu	Leu	Tyr
				485					490					495	
Val	Tyr	Pro	Gln	Arg	Leu	Asn	Phe	Val	Asn	Lys	Leu	Ala	Ser	Ala	Arg
			500					505					510		
Asn	Ile	Thr	Ile	Lys	Ile	Gln	Phe	Met	Cys	Gly	Glu	Asp	Ala	Ser	Asn
		515					520					525			
Ala	Met	Pro	Val	Ile	Phe	Gly	Lys	Ser	Ser	Gly	Pro	Glu	Phe	Leu	Gln
	530					535					540				
Glu	Val	Tyr	Thr	Ala	Val	Thr	Tyr	His	Asn	Lys	Ser	Pro	Asp	Phe	Tyr
545					550					555					560
Glu	Glu	Val	Lys	Ile	Lys	Leu	Pro	Ala	Lys	Leu	Thr	Val	Asn	His	His
			565						570					575	
Leu	Leu	Phe	Thr	Phe	Tyr	His	Ile	Ser	Cys	Gln	Gln	Lys	Gln	Gly	Ala
			580					585					590		
Ser	Val	Glu	Thr	Leu	Leu	Gly	Tyr	Ser	Trp	Leu	Pro	Ile	Leu	Leu	Asn
		595					600					605			
Glu	Arg	Leu	Gln	Thr	Gly	Ser	Tyr	Cys	Leu	Pro	Val	Ala	Leu	Glu	Lys
	610					615					620				
Leu	Pro	Pro	Asn	Tyr	Ser	Met	His	Ser	Ala	Glu	Lys	Val	Pro	Leu	Gln
625					630					635					640
Asn	Pro	Pro	Ile	Lys	Trp	Ala	Glu	Gly	His	Lys	Gly	Val	Phe	Asn	Ile
			645						650					655	
Glu	Val	Gln	Ala	Val	Ser	Ser	Val	His	Thr	Gln	Asp	Asn	His	Leu	Glu
			660					665					670		
Lys	Phe	Phe	Thr	Leu	Cys	His	Ser	Leu	Glu	Ser	Gln	Val	Thr	Phe	Pro
		675					680					685			

Ile Arg Val Leu Asp Gln Lys Ile Ser Glu Met Ala Leu Glu His Glu  
 690 695 700  
 Leu Lys Leu Ser Ile Ile Cys Leu Asn Ser Ser Arg Leu Glu Pro Leu  
 705 710 715 720  
 Val Leu Phe Leu His Leu Val Leu Asp Lys Leu Phe Gln Leu Ser Val  
 725 730 735  
 Gln Pro Met Val Ile Ala Gly Gln Thr Ala Asn Phe Ser Gln Phe Ala  
 740 745 750  
 Phe Glu Ser Val Val Ala Ile Ala Asn Ser Leu His Asn Ser Lys Asp  
 755 760 765  
 Leu Ser Lys Asp Gln His Gly Arg Asn Cys Leu Leu Ala Ser Tyr Val  
 770 775 780  
 His Tyr Val Phe Arg Leu Pro Glu Val Gln Arg Asp Val Pro Lys Ser  
 785 790 795 800  
 Gly Ala Pro Thr Ala Leu Leu Asp Pro Arg Ser Tyr His Thr Tyr Gly  
 805 810 815  
 Arg Thr Ser Ala Ala Ala Val Ser Ser Lys Leu Leu Gln Ala Arg Val  
 820 825 830  
 Met Ser Ser Ser Asn Pro Asp Leu Ala Gly Thr His Ser Ala Ala Asp  
 835 840 845  
 Glu Glu Val Lys Asn Ile Met Ser Ser Lys Ile Ala Asp Arg Asn Cys  
 850 855 860  
 Ser Arg Met Ser Tyr Tyr Cys Ser Gly Ser Ser Asp Ala Pro Ser Ser  
 865 870 875 880  
 Pro Ala Ala Pro Arg Pro Ala Ser Lys Lys His Phe His Glu Glu Leu  
 885 890 895  
 Ala Leu Gln Met Val Val Ser Thr Gly Met Val Lys Ser Met Ala Gln  
 900 905 910  
 His Val His Asn Met Asp Lys Arg Asp Ser Phe Arg Arg Thr Arg Phe  
 915 920 925  
 Ser Asp Arg Phe Met Asp Asp Ile Thr Thr Ile Val Asn Val Val Thr  
 930 935 940  
 Ser Glu Ile Ala Ala Leu Leu Val Lys Pro Gln Lys Glu Asn Glu Gln  
 945 950 955 960  
 Ala Glu Lys Met Asn Ile Ser Leu Ala Phe Phe Leu Tyr Asp Leu Leu  
 965 970 975  
 Ser Leu Met Asp Arg Gly Phe Val Phe Asn Leu Ile Arg His Tyr Cys  
 980 985 990  
 Ser Gln Leu Ser Ala Lys Leu Ser Asn Leu Pro Thr Leu Ile Ser Met  
 995 1000 1005

Arg Leu Glu Phe Leu Arg Ile Leu Cys Ser His Glu His Tyr Leu Asn  
 1010 1015 1020  
 Leu Asn Leu Phe Phe Met Asn Ala Asp Thr Ala Pro Thr Ser Pro Cys  
 1025 1030 1035 1040  
 Pro Ser Ile Ser Ser Gln Asn Ser Ser Ser Cys Ser Ser Phe Gln Asp  
 1045 1050 1055  
 Gln Lys Ile Ala Ser Met Phe Asp Leu Thr Ser Glu Tyr Arg Gln Gln  
 1060 1065 1070  
 His Phe Leu Thr Gly Leu Leu Phe Thr Glu Leu Ala Ala Ala Leu Asp  
 1075 1080 1085  
 Ala Glu Gly Glu Gly Ile Ser Lys Val Gln Arg Lys Ala Val Ser Ala  
 1090 1095 1100  
 Ile His Ser Leu Leu Ser Ser His Asp Leu Asp Pro Arg Cys Val Lys  
 1105 1110 1115 1120  
 Pro Glu Val Lys Val Lys Ile Ala Ala Leu Tyr Leu Pro Leu Val Gly  
 1125 1130 1135  
 Ile Ile Leu Asp Ala Leu Pro Gln Leu Cys Asp Phe Thr Val Ala Asp  
 1140 1145 1150  
 Thr Arg Arg Tyr Arg Thr Ser Gly Ser Asp Glu Glu Gln Glu Gly Ala  
 1155 1160 1165  
 Gly Ala Ile Asn Gln Asn Val Ala Leu Ala Ile Ala Gly Asn Asn Phe  
 1170 1175 1180  
 Asn Leu Lys Thr Ser Gly Ile Val Leu Ser Ser Leu Pro Tyr Lys Gln  
 1185 1190 1195 1200  
 Tyr Asn Met Leu Asn Ala Asp Thr Thr Arg Asn Leu Met Ile Cys Phe  
 1205 1210 1215  
 Leu Trp Ile Met Lys Asn Ala Asp Gln Ser Leu Ile Arg Lys Trp Ile  
 1220 1225 1230  
 Ala Asp Leu Pro Ser Thr Gln Leu Asn Arg Ile Leu Asp Leu Leu Phe  
 1235 1240 1245  
 Ile Cys Val Leu Cys Phe Glu Tyr Lys Gly Lys Gln Ser Ser Asp Lys  
 1250 1255 1260  
 Val Ser Thr Gln Val Leu Gln Lys Ser Arg Asp Val Lys Ala Arg Leu  
 1265 1270 1275 1280  
 Glu Glu Ala Leu Leu Arg Gly Glu Gly Ala Arg Gly Glu Met Met Arg  
 1285 1290 1295  
 Arg Arg Ala Pro Gly Asn Asp Arg Phe Pro Gly Leu Asn Glu Asn Leu  
 1300 1305 1310  
 Arg Trp Lys Lys Glu Gln Thr His Trp Arg Gln Ala Asn Glu Lys Leu  
 1315 1320 1325  
 Asp Lys Thr Lys Ala Glu Leu Asp Gln Glu Ala Leu Ile Ser Gly Asn

1330	1335	1340
Leu Ala Thr Glu Ala His Leu Ile Ile Leu Asp Met Gln Glu Asn Ile 1345	1350	1355 1360
Ile Gln Ala Ser Ser Ala Leu Asp Cys Lys Asp Ser Leu Leu Gly Gly 1365	1370	1375
Val Leu Arg Val Leu Val Asn Ser Leu Asn Cys Asp Gln Ser Thr Thr 1380	1385	1390
Tyr Leu Thr His Cys Phe Ala Thr Leu Arg Ala Leu Ile Ala Lys Phe 1395	1400	1405
Gly Asp Leu Leu Phe Glu Glu Glu Val Glu Gln Cys Phe Asp Leu Cys 1410	1415	1420
His Gln Val Leu His His Cys Ser Ser Ser Met Asp Val Thr Arg Ser 1425	1430	1435 1440
Gln Ala Cys Ala Thr Leu Tyr Leu Leu Met Arg Phe Ser Phe Gly Ala 1445	1450	1455
Thr Ser Asn Phe Ala Arg Val Lys Met Gln Val Thr Met Ser Leu Ala 1460	1465	1470
Ser Leu Val Gly Arg Ala Pro Asp Phe Asn Glu Glu His Leu Arg Arg 1475	1480	1485
Ser Leu Arg Thr Ile Leu Ala Tyr Ser Glu Glu Asp Thr Ala Met Gln 1490	1495	1500
Met Thr Pro Phe Pro Thr Gln Val Glu Glu Leu Leu Cys Asn Leu Asn 1505	1510	1515 1520
Ser Ile Leu Tyr Asp Thr Val Lys Met Arg Glu Phe Gln Glu Asp Pro 1525	1530	1535
Glu Met Leu Met Asp Leu Met Tyr Arg Ile Ala Lys Ser Tyr Gln Ala 1540	1545	1550
Ser Pro Asp Leu Arg Leu Thr Trp Leu Gln Asn Met Ala Glu Lys His 1555	1560	1565
Thr Lys Lys Lys Cys Tyr Thr Glu Ala Ala Met Cys Leu Val His Ala 1570	1575	1580
Ala Ala Leu Val Ala Glu Tyr Leu Ser Met Leu Glu Asp His Ser Tyr 1585	1590	1595 1600
Leu Pro Val Gly Ser Val Ser Phe Gln Asn Ile Ser Ser Asn Val Leu 1605	1610	1615
Glu Glu Ser Val Val Ser Glu Asp Thr Leu Ser Pro Asp Glu Asp Gly 1620	1625	1630
Val Cys Ala Gly Gln Tyr Phe Thr Glu Ser Gly Leu Val Gly Leu Leu 1635	1640	1645
Glu Gln Ala Ala Glu Leu Phe Ser Thr Gly Gly Leu Tyr Glu Thr Val 1650	1655	1660



Asn Glu Val Tyr Lys Leu Val Ile Pro Ile Leu Glu Ala His Arg Glu  
1665 1670 1675 1680

Phe Arg Lys Leu Thr Leu Thr His Ser Lys Leu Gln Arg Ala Phe Asp  
1685 1690 1695

Ser Ile Val Asn Lys Asp His Lys Arg Met Phe Gly Thr Tyr Phe Arg  
1700 1705 1710

Val Gly Phe Phe Gly Ser Lys Phe Gly Asp Leu Asp Glu Gln Glu Phe  
1715 1720 1725

Val Tyr Lys Glu Pro Ala Ile Thr Lys Leu Pro Glu Ile Ser His Arg  
1730 1735 1740

Leu Glu Ala Phe Tyr Gly Gln Cys Phe Gly Ala Glu Phe Val Glu Val  
1745 1750 1755 1760

Ile Lys Asp Ser Thr Pro Val Asp Lys Thr Lys Leu Asp Pro Asn Lys  
1765 1770 1775

Ala Tyr Ile Gln Ile Thr Phe Val Glu Pro Tyr Phe Asp Glu Tyr Glu  
1780 1785 1790

Met Lys Asp Arg Val Thr Tyr Phe Glu Lys Asn Phe Asn Leu Arg Arg  
1795 1800 1805

Phe Met Tyr Thr Thr Pro Phe Thr Leu Glu Gly Arg Pro Arg Gly Glu  
1810 1815 1820

Leu His Glu Gln Tyr Arg Arg Asn Thr Val Leu Thr Thr Met His Ala  
1825 1830 1835 1840

Phe Pro Tyr Ile Lys Thr Arg Ile Ser Val Ile Gln Lys Glu Glu Phe  
1845 1850 1855

Val Leu Thr Pro Ile Glu Val Ala Ile Glu Asp Met Lys Lys Lys Thr  
1860 1865 1870

Leu Gln Leu Ala Val Ala Ile Asn Gln Glu Pro Pro Asp Ala Lys Met  
1875 1880 1885

Leu Gln Met Val Leu Gln Gly Ser Val Gly Ala Thr Val Asn Gln Gly  
1890 1895 1900

Pro Leu Glu Val Ala Gln Val Phe Leu Ala Glu Ile Pro Ala Asp Pro  
1905 1910 1915 1920

Lys Leu Tyr Arg His His Asn Lys Leu Arg Leu Cys Phe Lys Glu Phe  
1925 1930 1935

Ile Met Arg Cys Gly Glu Ala Val Glu Lys Asn Lys Arg Leu Ile Thr  
1940 1945 1950

Ala Asp Gln Arg Glu Tyr Gln Gln Glu Leu Lys Lys Asn Tyr Asn Lys  
1955 1960 1965

Leu Lys Glu Asn Leu Arg Pro Met Ile Glu Arg Lys Ile Pro Glu Leu  
1970 1975 1980

Tyr Lys Pro Ile Phe Arg Val Glu Ser Gln Lys Arg Asp Ser Phe His  
1985 1990 1995 2000

Arg Ser Ser Phe Arg Lys Cys Glu Thr Gln Leu Ser Gln Gly Ser  
2005 2010 2015

<210> 107

<211> 2090

<212> PRT

<213> Homo sapiens

<220>

<223> human CLASP-3

<400> 107

Met Ala Glu Arg Arg Ala Phe Ala Gln Lys Ile Ser Arg Thr Val Ala  
1 5 10 15

Ala Glu Val Arg Lys Gln Ile Ser Gly Gln Tyr Ser Gly Ser Pro Gln  
20 25 30

Leu Leu Lys Asn Leu Asn Ile Val Gly Asn Ile Ser His His Thr Thr  
35 40 45

Val Pro Leu Thr Glu Ala Val Asp Pro Val Asp Leu Glu Asp Tyr Leu  
50 55 60

Ile Thr His Pro Leu Ala Val Asp Ser Gly Pro Leu Arg Asp Leu Ile  
65 70 75 80

Glu Phe Pro Pro Asp Asp Ile Glu Val Val Tyr Ser Pro Arg Asp Cys  
85 90 95

Arg Thr Leu Val Ser Ala Val Pro Glu Glu Ser Glu Met Asp Pro His  
100 105 110

Val Arg Asp Cys Ile Arg Ser Tyr Thr Glu Asp Trp Ala Ile Val Ile  
115 120 125

Arg Lys Tyr His Lys Leu Gly Thr Gly Phe Asn Pro Asn Thr Leu Asp  
130 135 140

Lys Gln Lys Glu Arg Gln Lys Gly Leu Pro Lys Gln Val Phe Glu Ser  
145 150 155 160

Asp Glu Ala Pro Asp Gly Asn Ser Tyr Gln Asp Asp Gln Asp Asp Leu  
165 170 175

Lys Arg Arg Ser Met Ser Ile Asp Asp Thr Pro Arg Gly Ser Trp Ala  
180 185 190

Cys Ser Ile Phe Asp Leu Lys Asn Ser Leu Pro Asp Ala Leu Leu Pro  
195 200 205

Asn Leu Leu Asp Arg Thr Pro Asn Glu Glu Ile Asp Arg Gln Asn Asp  
210 215 220

Asp Gln Arg Lys Ser Asn Arg His Lys Glu Leu Phe Ala Leu His Pro  
225 230 235 240

Ser Pro Asp Glu Glu Glu Pro Ile Glu Arg Leu Ser Val Pro Asp Ile  
 245 250 255  
 Pro Lys Glu His Phe Gly Gln Arg Leu Leu Val Lys Cys Leu Ser Leu  
 260 265 270  
 Lys Phe Glu Ile Glu Ile Glu Pro Ile Phe Ala Ser Leu Ala Leu Tyr  
 275 280 285  
 Asp Val Lys Glu Lys Lys Lys Ile Ser Glu Asn Phe Tyr Phe Asp Leu  
 290 295 300  
 Asn Ser Glu Gln Met Lys Gly Leu Leu Arg Pro His Val Pro Pro Ala  
 305 310 315 320  
 Ala Ile Thr Thr Leu Ala Arg Ser Ala Ile Phe Ser Ile Thr Tyr Pro  
 325 330 335  
 Ser Gln Asp Val Phe Leu Val Ile Lys Leu Glu Lys Val Leu Gln Gln  
 340 345 350  
 Gly Asp Ile Gly Glu Cys Ala Glu Pro Tyr Met Ile Phe Lys Glu Ala  
 355 360 365  
 Asp Ala Thr Lys Asn Lys Glu Lys Leu Glu Lys Leu Lys Ser Gln Ala  
 370 375 380  
 Asp Gln Phe Cys Gln Arg Leu Gly Lys Tyr Arg Met Pro Phe Ala Trp  
 385 390 395 400  
 Thr Ala Ile His Leu Met Asn Ile Val Ser Ser Ala Gly Ser Leu Glu  
 405 410 415  
 Arg Asp Ser Thr Glu Val Glu Ile Ser Thr Gly Glu Arg Lys Gly Ser  
 420 425 430  
 Trp Ser Glu Arg Arg Asn Ser Ser Ile Val Gly Arg Arg Ser Leu Glu  
 435 440 445  
 Arg Thr Thr Ser Gly Asp Asp Ala Cys Asn Leu Thr Ser Phe Arg Pro  
 450 455 460  
 Ala Thr Leu Thr Val Thr Asn Phe Phe Lys Gln Glu Gly Asp Arg Leu  
 465 470 475 480  
 Ser Asp Glu Asp Leu Tyr Lys Phe Leu Ala Asp Met Arg Arg Pro Ser  
 485 490 495  
 Ser Val Leu Arg Arg Leu Arg Pro Ile Thr Ala Gln Leu Lys Ile Asp  
 500 505 510  
 Ile Ser Pro Ala Pro Glu Asn Pro His Tyr Cys Leu Thr Pro Glu Leu  
 515 520 525  
 Leu Gln Val Lys Leu Tyr Pro Asp Ser Arg Val Arg Pro Thr Arg Glu  
 530 535 540  
 Ile Leu Glu Phe Pro Ala Arg Asp Val Tyr Val Pro Asn Thr Thr Tyr  
 545 550 555 560  
 Arg Asn Leu Leu Tyr Ile Tyr Pro Gln Ser Leu Asn Phe Ala Asn Arg

565										570					575				
Gln	Gly	Ser	Ala	Arg	Asn	Ile	Thr	Val	Lys	Val	Gln	Phe	Met	Tyr	Gly				
			580					585					590						
Glu	Asp	Pro	Ser	Asn	Ala	Met	Pro	Val	Ile	Phe	Gly	Lys	Ser	Ser	Cys				
		595					600					605							
Ser	Glu	Phe	Ser	Lys	Glu	Ala	Tyr	Thr	Ala	Val	Val	Tyr	His	Asn	Arg				
	610					615					620								
Ser	Pro	Asp	Phe	His	Glu	Glu	Ile	Lys	Val	Lys	Leu	Pro	Ala	Thr	Leu				
625					630					635					640				
Thr	Asp	His	His	His	Leu	Leu	Phe	Thr	Phe	Tyr	His	Val	Ser	Cys	Gln				
				645					650					655					
Gln	Lys	Gln	Asn	Thr	Pro	Leu	Glu	Thr	Pro	Val	Gly	Tyr	Thr	Trp	Ile				
			660					665					670						
Pro	Met	Leu	Gln	Asn	Gly	Arg	Leu	Lys	Thr	Gly	Gln	Phe	Cys	Leu	Pro				
		675					680					685							
Val	Ser	Leu	Glu	Lys	Pro	Pro	Gln	Ala	Tyr	Ser	Val	Leu	Ser	Pro	Glu				
	690					695					700								
Val	Pro	Leu	Pro	Gly	Met	Lys	Trp	Val	Asp	Asn	His	Lys	Gly	Val	Phe				
705					710				715						720				
Asn	Val	Glu	Val	Val	Ala	Val	Ser	Ser	Ile	His	Thr	Gln	Asp	Pro	Tyr				
				725					730					735					
Leu	Asp	Lys	Phe	Phe	Ala	Leu	Val	Asn	Ala	Leu	Asp	Glu	His	Leu	Phe				
			740					745					750						
Pro	Val	Arg	Ile	Gly	Asp	Met	Arg	Ile	Met	Glu	Asn	Asn	Leu	Glu	Asn				
		755					760					765							
Glu	Leu	Lys	Ser	Ser	Ile	Ser	Ala	Leu	Asn	Ser	Ser	Gln	Leu	Glu	Pro				
	770					775					780								
Val	Val	Arg	Phe	Leu	His	Leu	Leu	Leu	Asp	Lys	Leu	Ile	Leu	Leu	Val				
785					790				795						800				
Ile	Arg	Pro	Pro	Val	Ile	Ala	Gly	Gln	Ile	Val	Asn	Leu	Gly	Gln	Ala				
				805				810						815					
Ser	Phe	Glu	Ala	Met	Ala	Ser	Ile	Ile	Asn	Arg	Leu	His	Lys	Asn	Leu				
			820					825					830						
Glu	Gly	Asn	His	Asp	Gln	His	Gly	Arg	Asn	Ser	Leu	Leu	Ala	Ser	Tyr				
		835					840					845							
Ile	His	Tyr	Val	Phe	Arg	Leu	Pro	Asn	Thr	Tyr	Pro	Asn	Ser	Ser	Ser				
	850					855					860								
Pro	Gly	Pro	Gly	Gly	Leu	Gly	Gly	Ser	Val	His	Tyr	Ala	Thr	Met	Ala				
865					870						875				880				
Arg	Ser	Ala	Val	Arg	Pro	Ala	Ser	Leu	Asn	Leu	Asn	Arg	Ser	Arg	Ser				
				885					890					895					

Leu Ser Asn Ser Asn Pro Asp Ile Ser Gly Thr Pro Thr Ser Pro Asp  
 900 905 910  
 Asp Glu Val Arg Ser Ile Ile Gly Ser Lys Gly Leu Asp Arg Ser Asn  
 915 920 925  
 Ser Trp Val Asn Thr Gly Gly Pro Lys Ala Ala Pro Trp Gly Ser Asn  
 930 935 940  
 Pro Ser Pro Ser Ala Glu Ser Thr Gln Ala Met Asp Arg Ser Cys Asn  
 945 950 955 960  
 Arg Met Ser Ser His Thr Glu Thr Ser Ser Phe Leu Gln Thr Leu Thr  
 965 970 975  
 Gly Arg Leu Pro Thr Lys Lys Leu Phe His Glu Glu Leu Ala Leu Gln  
 980 985 990  
 Trp Val Val Cys Ser Gly Ser Val Arg Glu Ser Ala Leu Gln Gln Ala  
 995 1000 1005  
 Trp Phe Phe Phe Glu Leu Met Val Lys Ser Met Val His His Leu Tyr  
 1010 1015 1020  
 Phe Asn Asp Lys Leu Glu Ala Pro Arg Lys Ser Arg Phe Pro Glu Arg  
 1025 1030 1035 1040  
 Phe Met Asp Asp Ile Ala Ala Leu Val Ser Thr Ile Ala Ser Asp Ile  
 1045 1050 1055  
 Val Ser Arg Phe Gln Lys Asp Thr Glu Met Val Glu Arg Leu Asn Thr  
 1060 1065 1070  
 Ser Leu Ala Phe Phe Leu Asn Asp Leu Leu Ser Val Met Asp Arg Gly  
 1075 1080 1085  
 Phe Val Phe Ser Leu Ile Lys Ser Cys Tyr Lys Gln Val Ser Ser Lys  
 1090 1095 1100  
 Leu Tyr Ser Leu Pro Asn Pro Ser Val Leu Val Ser Leu Arg Leu Asp  
 1105 1110 1115 1120  
 Phe Leu Arg Ile Ile Cys Ser His Glu His Tyr Val Thr Leu Asn Leu  
 1125 1130 1135  
 Pro Cys Ser Leu Leu Thr Pro Pro Ala Ser Pro Ser Pro Ser Val Ser  
 1140 1145 1150  
 Ser Ala Thr Ser Gln Ser Ser Gly Phe Ser Thr Asn Val Gln Asp Gln  
 1155 1160 1165  
 Lys Ile Ala Asn Met Phe Glu Leu Ser Val Pro Phe Arg Gln Gln His  
 1170 1175 1180  
 Tyr Leu Ala Gly Leu Val Leu Thr Glu Leu Ala Val Ile Leu Asp Pro  
 1185 1190 1195 1200  
 Asp Ala Glu Gly Leu Phe Gly Leu His Lys Lys Val Ile Asn Met Val  
 1205 1210 1215

His Asn Leu Leu Ser Ser His Asp Ser Asp Pro Arg Tyr Ser Asp Pro  
 1220 1225 1230  
 Gln Ile Lys Ala Arg Val Ala Met Leu Tyr Leu Pro Leu Ile Gly Ile  
 1235 1240 1245  
 Ile Met Glu Thr Val Pro Gln Leu Tyr Asp Phe Thr Glu Thr His Asn  
 1250 1255 1260  
 Gln Arg Gly Arg Pro Ile Cys Ile Ala Thr Asp Asp Tyr Glu Ser Glu  
 1265 1270 1275 1280  
 Ser Gly Ser Met Ile Ser Gln Thr Val Ala Met Ala Ile Ala Gly Thr  
 1285 1290 1295  
 Ser Val Pro Gln Leu Thr Arg Pro Gly Ser Phe Leu Leu Thr Ser Thr  
 1300 1305 1310  
 Ser Gly Arg Gln His Thr Thr Phe Ser Ala Glu Ser Ser Arg Ser Leu  
 1315 1320 1325  
 Leu Ile Cys Leu Leu Trp Val Leu Lys Asn Ala Asp Glu Thr Val Leu  
 1330 1335 1340  
 Gln Lys Trp Phe Thr Asp Leu Ser Val Leu Gln Leu Asn Arg Leu Leu  
 1345 1350 1355 1360  
 Asp Leu Leu Tyr Leu Cys Val Ser Cys Phe Glu Tyr Lys Gly Lys Lys  
 1365 1370 1375  
 Val Phe Glu Arg Met Asn Ser Leu Thr Phe Lys Lys Ser Lys Asp Met  
 1380 1385 1390  
 Arg Ala Lys Leu Glu Glu Ala Ile Leu Gly Ser Ile Gly Ala Arg Gln  
 1395 1400 1405  
 Glu Met Val Arg Arg Ser Arg Gly Gln Leu Glu Arg Ser Pro Ser Gly  
 1410 1415 1420  
 Ser Ala Phe Gly Ser Gln Glu Asn Leu Arg Trp Arg Lys Asp Met Thr  
 1425 1430 1435 1440  
 His Trp Arg Gln Asn Thr Glu Lys Leu Asp Lys Ser Arg Ala Glu Ile  
 1445 1450 1455  
 Glu His Glu Ala Leu Ile Asp Gly Asn Leu Ala Thr Glu Ala Asn Leu  
 1460 1465 1470  
 Ile Ile Leu Asp Thr Leu Glu Ile Val Val Gln Thr Val Ser Val Thr  
 1475 1480 1485  
 Glu Ser Lys Glu Ser Ile Leu Gly Gly Val Leu Lys Val Leu Leu His  
 1490 1495 1500  
 Ser Met Ala Cys Asn Gln Ser Ala Val Tyr Leu Gln His Cys Phe Ala  
 1505 1510 1515 1520  
 Thr Gln Arg Ala Leu Val Ser Lys Phe Pro Glu Leu Leu Phe Glu Glu  
 1525 1530 1535  
 Glu Thr Glu Gln Cys Ala Asp Leu Cys Leu Arg Leu Leu Arg His Cys

1540	1545	1550
Ser Ser Ser Ile Gly Thr Ile Arg Ser His Pro Ser Ala Ser Leu Tyr 1555	1560	1565
Leu Leu Met Arg Gln Asn Phe Glu Ile Gly Asn Asn Phe Ala Arg Val 1570	1575	1580
Lys Met Gln Val Pro Met Ser Leu Ser Ser Leu Val Gly Thr Ser Gln 1585	1590	1595 1600
Asn Phe Asn Glu Glu Phe Leu Arg Arg Ser Leu Lys Thr Ile Leu Thr 1605	1610	1615
Tyr Ala Glu Glu Asp Leu Glu Leu Arg Glu Thr Thr Phe Pro Asp Gln 1620	1625	1630
Val Gln Asp Leu Val Phe Asn Leu His Met Ile Leu Ser Asp Thr Val 1635	1640	1645
Lys Met Lys Glu His Gln Glu Asp Pro Glu Met Leu Ile Asp Leu Met 1650	1655	1660
Tyr Arg Ile Ala Lys Gly Tyr Gln Thr Ser Pro Glu Arg Leu Thr Trp 1665	1670	1675 1680
Leu Gln Asn Met Ala Gly Lys His Ser Glu Arg Ser Asn His Ala Glu 1685	1690	1695
Ala Ala Gln Cys Leu Val His Ser Ala Ala Leu Val Ala Glu Tyr Leu 1700	1705	1710
Ser Met Leu Glu Asp Arg Lys Tyr Leu Pro Val Gly Cys Val Thr Phe 1715	1720	1725
Gln Asn Ile Ser Ser Asn Val Leu Glu Glu Ser Ala Val Ser Asp Asp 1730	1735	1740
Val Val Ser Pro Asp Glu Glu Gly Ile Cys Ser Gly Lys Tyr Phe Thr 1745	1750	1755 1760
Glu Ser Gly Leu Val Gly Leu Leu Glu Gln Ala Ala Ala Ser Phe Ser 1765	1770	1775
Met Ala Gly Met Tyr Glu Ala Val Asn Glu Val Tyr Lys Val Leu Ile 1780	1785	1790
Pro Ile His Glu Ala Asn Arg Asp Ala Lys Lys Leu Ser Thr Ile His 1795	1800	1805
Gly Lys Leu Gln Glu Ala Phe Ser Lys Ile Val His Gln Ser Thr Gly 1810	1815	1820
Trp Glu Arg Met Phe Gly Thr Tyr Phe Arg Val Gly Phe Tyr Gly Thr 1825	1830	1835 1840
Lys Phe Gly Asp Leu Asp Glu Gln Glu Phe Val Tyr Lys Glu Pro Ala 1845	1850	1855
Ile Thr Lys Leu Ala Glu Ile Ser His Arg Leu Glu Gly Phe Tyr Gly 1860	1865	1870

Glu Arg Phe Gly Glu Asp Val Val Glu Val Ile Lys Asp Ser Asn Pro  
 1875 1880 1885

Val Asp Lys Cys Lys Leu Asp Pro Asn Lys Ala Tyr Ile Gln Ile Thr  
 1890 1895 1900

Tyr Val Glu Pro Tyr Phe Asp Thr Tyr Glu Met Lys Asp Arg Ile Thr  
 1905 1910 1915 1920

Tyr Phe Asp Lys Asn Tyr Asn Leu Arg Arg Phe Met Tyr Cys Thr Pro  
 1925 1930 1935

Phe Thr Leu Asp Gly Arg Ala His Gly Glu Leu His Glu Gln Phe Lys  
 1940 1945 1950

Arg Lys Thr Ile Leu Thr Thr Ser His Ala Phe Pro Tyr Ile Lys Thr  
 1955 1960 1965

Arg Val Asn Val Thr His Lys Glu Glu Ile Ile Leu Thr Pro Ile Glu  
 1970 1975 1980

Val Ala Ile Glu Asp Met Gln Lys Lys Thr Gln Glu Leu Ala Phe Ala  
 1985 1990 1995 2000

Thr His Gln Asp Pro Ala Asp Pro Lys Met Leu Gln Met Val Leu Gln  
 2005 2010 2015

Gly Ser Val Gly Thr Thr Val Asn Gln Gly Pro Leu Glu Val Ala Gln  
 2020 2025 2030

Val Phe Leu Ser Glu Ile Pro Ser Asp Pro Lys Leu Phe Arg His His  
 2035 2040 2045

Asn Lys Leu Arg Leu Cys Phe Lys Asp Phe Thr Lys Arg Cys Glu Asp  
 2050 2055 2060

Ala Leu Arg Lys Asn Lys Ser Leu Ile Gly Pro Val Gln Lys Glu Tyr  
 2065 2070 2075 2080

Gln Arg Glu Leu Gly Lys Leu Ser Ser Pro  
 2085 2090

<210> 108

<211> 1980

<212> PRT

<213> Homo sapiens

<220>

<223> human CLASP-2

<400> 108

Met Leu Leu Phe Pro Tyr Asp Asp Phe Gln Thr Ala Ile Leu Arg Arg  
 1 5 10 15

Gln Gly Arg Tyr Ile Cys Ser Thr Val Pro Ala Lys Ala Glu Glu Glu  
 20 25 30

Ala Gln Ser Leu Phe Val Thr Glu Cys Ile Lys Thr Tyr Asn Ser Asp  
 35 40 45



Trp His Leu Val Asn Tyr Lys Tyr Glu Asp Tyr Ser Gly Glu Phe Arg  
 50 55 60  
 Gln Leu Pro Asn Lys Val Val Lys Leu Asp Lys Leu Pro Val His Val  
 65 70 75 80  
 Tyr Glu Val Asp Glu Glu Val Asp Lys Asp Glu Asp Ala Ala Ser Leu  
 85 90 95  
 Gly Ser Gln Lys Gly Gly Ile Thr Lys His Gly Trp Leu Tyr Lys Gly  
 100 105 110  
 Asn Met Asn Ser Ala Ile Ser Val Thr Met Arg Ser Phe Lys Arg Arg  
 115 120 125  
 Phe Phe His Leu Ile Gln Leu Gly Asp Gly Ser Tyr Asn Leu Asn Phe  
 130 135 140  
 Tyr Lys Asp Glu Lys Ile Ser Lys Glu Pro Lys Gly Ser Ile Phe Leu  
 145 150 155 160  
 Asp Ser Cys Met Gly Val Val Gln Asn Asn Lys Val Arg Arg Phe Ala  
 165 170 175  
 Phe Glu Leu Lys Met Gln Asp Lys Ser Ser Tyr Leu Leu Ala Ala Asp  
 180 185 190  
 Ser Glu Val Glu Met Glu Glu Trp Ile Thr Ile Leu Asn Lys Ile Leu  
 195 200 205  
 Gln Leu Asn Phe Glu Ala Ala Met Gln Glu Lys Arg Asn Gly Asp Ser  
 210 215 220  
 His Glu Asp Asp Glu Gln Ser Lys Leu Glu Gly Ser Gly Ser Gly Leu  
 225 230 235 240  
 Asp Ser Tyr Leu Pro Glu Leu Ala Lys Ser Ala Arg Glu Ala Glu Ile  
 245 250 255  
 Lys Leu Lys Ser Glu Ser Arg Val Lys Leu Phe Tyr Leu Asp Pro Asp  
 260 265 270  
 Ala Gln Lys Leu Asp Phe Ser Ser Ala Glu Pro Glu Val Lys Ser Phe  
 275 280 285  
 Glu Glu Lys Phe Gly Lys Arg Ile Leu Val Lys Cys Asn Asp Leu Ser  
 290 295 300  
 Phe Asn Leu Gln Cys Cys Val Ala Glu Asn Glu Gly Pro Thr Thr  
 305 310 315 320  
 Asn Val Glu Pro Phe Phe Val Thr Leu Ser Leu Phe Asp Ile Lys Tyr  
 325 330 335  
 Asn Arg Lys Ile Ser Ala Asp Phe His Val Asp Leu Asn His Phe Ser  
 340 345 350  
 Val Arg Gln Met Leu Ala Thr Thr Ser Pro Ala Leu Met Asn Gly Ser  
 355 360 365

Gly Gln Ser Pro Ser Val Leu Lys Gly Ile Leu His Glu Ala Ala Met  
 370 375 380  
 Gln Tyr Pro Lys Gln Gly Ile Phe Ser Val Thr Cys Pro His Pro Asp  
 385 390 395 400  
 Ile Phe Leu Val Ala Arg Ile Glu Lys Val Leu Gln Gly Ser Ile Thr  
 405 410 415  
 His Cys Ala Glu Pro Tyr Met Lys Ser Ser Asp Ser Ser Lys Val Ala  
 420 425 430  
 Gln Lys Val Leu Lys Asn Ala Lys Gln Ala Cys Gln Arg Leu Gly Gln  
 435 440 445  
 Tyr Arg Met Pro Phe Ala Trp Ala Ala Arg Thr Leu Phe Lys Asp Ala  
 450 455 460  
 Ser Gly Asn Leu Asp Lys Asn Ala Arg Phe Ser Ala Ile Tyr Arg Gln  
 465 470 475 480  
 Asp Ser Asn Lys Leu Ser Asn Asp Asp Met Leu Lys Leu Leu Ala Asp  
 485 490 495  
 Phe Arg Lys Pro Glu Lys Met Ala Lys Leu Pro Val Ile Leu Gly Asn  
 500 505 510  
 Leu Asp Ile Thr Ile Asp Asn Val Ser Ser Asp Phe Pro Asn Tyr Val  
 515 520 525  
 Asn Ser Ser Tyr Ile Pro Thr Lys Gln Phe Glu Thr Cys Ser Lys Thr  
 530 535 540  
 Pro Ile Thr Phe Glu Val Glu Glu Phe Val Pro Cys Ile Pro Lys His  
 545 550 555 560  
 Thr Gln Pro Tyr Thr Ile Tyr Thr Asn His Leu Tyr Val Tyr Pro Lys  
 565 570 575  
 Tyr Leu Lys Tyr Asp Ser Gln Lys Ser Phe Ala Lys Ala Arg Asn Ile  
 580 585 590  
 Ala Ile Cys Ile Glu Phe Lys Asp Ser Asp Glu Glu Asp Ser Gln Pro  
 595 600 605  
 Leu Lys Cys Ile Tyr Gly Arg Pro Gly Gly Pro Val Phe Thr Arg Ser  
 610 615 620  
 Ala Phe Ala Ala Val Leu His His His Gln Asn Pro Glu Phe Tyr Asp  
 625 630 635 640  
 Glu Ile Lys Ile Glu Leu Pro Thr Gln Leu His Glu Lys His His Leu  
 645 650 655  
 Leu Leu Thr Phe Phe His Val Ser Cys Asp Asn Ser Ser Lys Gly Ser  
 660 665 670  
 Thr Lys Lys Arg Asp Val Val Glu Thr Gln Val Gly Tyr Ser Trp Leu  
 675 680 685  
 Pro Leu Leu Lys Asp Gly Arg Val Val Thr Ser Glu Gln His Ile Pro

690					695					700					
Val	Ser	Ala	Asn	Leu	Pro	Ser	Gly	His	Leu	Gly	Tyr	Gln	Glu	Leu	Gly
705					710					715					720
Met	Gly	Arg	His	Tyr	Gly	Pro	Glu	Ile	Lys	Trp	Val	Asp	Gly	Gly	Lys
				725					730					735	
Pro	Leu	Leu	Lys	Ile	Ser	Thr	His	Leu	Val	Ser	Thr	Val	Tyr	Thr	Gln
			740					745					750		
Asp	Gln	His	Leu	His	Asn	Phe	Phe	Gln	Tyr	Cys	Gln	Lys	Thr	Glu	Ser
		755					760					765			
Gly	Ala	Gln	Ala	Leu	Gly	Asn	Glu	Leu	Val	Lys	Tyr	Leu	Lys	Ser	Leu
	770					775					780				
His	Ala	Met	Glu	Gly	His	Val	Met	Ile	Ala	Phe	Leu	Pro	Thr	Ile	Leu
785					790					795					800
Asn	Gln	Leu	Phe	Arg	Val	Leu	Thr	Arg	Ala	Thr	Gln	Glu	Glu	Val	Ala
			805						810					815	
Val	Asn	Val	Thr	Arg	Val	Ile	Ile	His	Val	Val	Ala	Gln	Cys	His	Glu
			820					825					830		
Glu	Gly	Leu	Glu	Ser	His	Leu	Arg	Ser	Tyr	Val	Lys	Tyr	Ala	Tyr	Lys
		835					840					845			
Ala	Glu	Pro	Tyr	Val	Ala	Ser	Glu	Tyr	Lys	Thr	Val	His	Glu	Glu	Leu
	850					855					860				
Thr	Lys	Ser	Met	Thr	Thr	Ile	Leu	Lys	Pro	Ser	Ala	Asp	Phe	Leu	Thr
865					870					875					880
Ser	Asn	Lys	Leu	Leu	Arg	Tyr	Ser	Trp	Phe	Phe	Phe	Asp	Val	Leu	Ile
				885					890					895	
Lys	Ser	Met	Ala	Gln	His	Leu	Ile	Glu	Asn	Ser	Lys	Val	Lys	Leu	Leu
			900					905					910		
Arg	Asn	Gln	Arg	Phe	Pro	Ala	Ser	Tyr	His	His	Ala	Ala	Glu	Thr	Val
		915					920					925			
Val	Asn	Met	Leu	Met	Pro	His	Ile	Thr	Gln	Lys	Phe	Gly	Asp	Asn	Pro
	930					935					940				
Glu	Ala	Ser	Lys	Asn	Ala	Asn	His	Ser	Leu	Ala	Val	Phe	Ile	Lys	Arg
945					950					955					960
Cys	Phe	Thr	Phe	Met	Asp	Arg	Gly	Phe	Val	Phe	Lys	Gln	Ile	Asn	Asn
				965					970					975	
Tyr	Ile	Ser	Cys	Phe	Ala	Pro	Gly	Asp	Pro	Lys	Thr	Leu	Phe	Glu	Tyr
			980					985					990		
Lys	Phe	Glu	Phe	Leu	Arg	Val	Val	Cys	Asn	His	Glu	His	Tyr	Ile	Pro
		995					1000					1005			
Leu	Asn	Leu	Pro	Met	Pro	Phe	Gly	Lys	Gly	Arg	Ile	Gln	Arg	Tyr	Gln
	1010					1015					1020				

Asp Leu Gln Leu Asp Tyr Ser Leu Thr Asp Glu Phe Cys Arg Asn His  
 1025 1030 1035 1040  
 Phe Leu Val Gly Leu Leu Leu Arg Glu Val Gly Thr Ala Leu Gln Glu  
 1045 1050 1055  
 Phe Arg Glu Val Arg Leu Ile Ala Ile Ser Val Leu Lys Asn Leu Leu  
 1060 1065 1070  
 Ile Lys His Ser Phe Asp Asp Arg Tyr Ala Ser Arg Ser His Gln Ala  
 1075 1080 1085  
 Arg Ile Ala Thr Leu Tyr Leu Pro Leu Phe Gly Leu Leu Ile Glu Asn  
 1090 1095 1100  
 Val Gln Arg Ile Asn Val Arg Asp Val Ser Pro Phe Pro Val Asn Ala  
 1105 1110 1115 1120  
 Gly Met Thr Val Lys Asp Glu Ser Leu Ala Leu Pro Ala Val Asn Pro  
 1125 1130 1135  
 Leu Val Thr Pro Gln Lys Gly Ser Thr Leu Asp Asn Ser Leu His Lys  
 1140 1145 1150  
 Asp Leu Leu Gly Ala Ile Ser Gly Ile Ala Ser Pro Tyr Thr Thr Ser  
 1155 1160 1165  
 Thr Pro Asn Ile Asn Ser Val Arg Asn Ala Asp Ser Arg Gly Ser Leu  
 1170 1175 1180  
 Ile Ser Thr Asp Ser Gly Asn Ser Leu Pro Glu Arg Asn Ser Glu Lys  
 1185 1190 1195 1200  
 Ser Asn Ser Leu Asp Lys His Gln Gln Ser Ser Thr Leu Gly Asn Ser  
 1205 1210 1215  
 Val Val Arg Cys Asp Lys Leu Asp Gln Ser Glu Ile Lys Ser Leu Leu  
 1220 1225 1230  
 Met Cys Phe Leu Tyr Ile Leu Lys Ser Met Ser Asp Asp Ala Leu Phe  
 1235 1240 1245  
 Thr Tyr Trp Asn Lys Ala Ser Thr Ser Glu Leu Met Asp Phe Phe Thr  
 1250 1255 1260  
 Ile Ser Glu Val Cys Leu His Gln Phe Gln Tyr Met Gly Lys Arg Tyr  
 1265 1270 1275 1280  
 Ile Ala Arg Asn Gln Glu Gly Leu Gly Pro Ile Val His Asp Arg Lys  
 1285 1290 1295  
 Ser Gln Thr Leu Pro Val Ser Arg Asn Arg Thr Gly Met Met His Ala  
 1300 1305 1310  
 Arg Leu Gln Gln Leu Gly Ser Leu Asp Asn Ser Leu Thr Phe Asn His  
 1315 1320 1325  
 Ser Tyr Gly His Ser Asp Ala Asp Val Leu His Gln Ser Leu Leu Glu  
 1330 1335 1340

Ala Asn Ile Ala Thr Glu Val Cys Leu Thr Ala Leu Asp Thr Leu Ser  
1345 1350 1355 1360

Leu Phe Thr Leu Ala Phe Lys Asn Gln Leu Leu Ala Asp His Gly His  
1365 1370 1375

Asn Pro Leu Met Lys Lys Val Phe Asp Val Tyr Leu Cys Phe Leu Gln  
1380 1385 1390

Lys His Gln Ser Glu Thr Ala Leu Lys Asn Val Phe Thr Ala Leu Arg  
1395 1400 1405

Ser Leu Ile Tyr Lys Phe Pro Ser Thr Phe Tyr Glu Gly Arg Ala Asp  
1410 1415 1420

Met Cys Ala Ala Leu Cys Tyr Glu Ile Leu Lys Cys Cys Asn Ser Lys  
1425 1430 1435 1440

Leu Ser Ser Ile Arg Thr Glu Ala Ser Gln Leu Leu Tyr Phe Leu Met  
1445 1450 1455

Arg Asn Asn Phe Asp Tyr Thr Gly Lys Lys Ser Phe Val Arg Thr His  
1460 1465 1470

Leu Gln Val Ile Ile Ser Val Ser Gln Leu Ile Ala Asp Val Val Gly  
1475 1480 1485

Ile Gly Glu Thr Arg Phe Gln Gln Ser Leu Ser Ile Ile Asn Asn Cys  
1490 1495 1500

Ala Asn Ser Asp Arg Leu Ile Lys His Thr Ser Phe Ser Ser Asp Val  
1505 1510 1515 1520

Lys Asp Leu Thr Lys Arg Ile Arg Thr Val Leu Met Ala Thr Ala Gln  
1525 1530 1535

Met Lys Glu His Glu Asn Asp Pro Glu Met Leu Val Asp Leu Gln Tyr  
1540 1545 1550

Ser Leu Ala Lys Ser Tyr Ala Ser Thr Pro Glu Leu Arg Lys Thr Trp  
1555 1560 1565

Leu Asp Ser Met Ala Arg Ile His Val Lys Asn Gly Asp Leu Ser Glu  
1570 1575 1580

Ala Ala Met Cys Tyr Val His Val Thr Ala Leu Val Ala Glu Tyr Leu  
1585 1590 1595 1600

Thr Arg Lys Gly Val Phe Arg Gln Gly Cys Thr Ala Phe Arg Val Ile  
1605 1610 1615

Thr Pro Asn Ile Asp Glu Glu Ala Ser Met Met Glu Asp Val Gly Met  
1620 1625 1630

Gln Asp Val His Phe Asn Glu Asp Val Leu Met Glu Leu Leu Glu Gln  
1635 1640 1645

Cys Ala Asp Gly Leu Trp Lys Ala Glu Arg Tyr Glu Leu Ile Ala Asp  
1650 1655 1660

Ile Tyr Lys Leu Ile Ile Pro Ile Tyr Glu Lys Arg Arg Asp Phe Phe

1665	1670	1675	1680
Glu Asp Glu Asp Gly Lys Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr	1685	1690	1695
Pro Leu Ser Glu Ile Ser Gln Arg Leu Leu Lys Leu Tyr Ser Asp Lys	1700	1705	1710
Phe Gly Ser Glu Asn Val Lys Met Ile Gln Asp Ser Gly Lys Val Asn	1715	1720	1725
Pro Lys Asp Leu Asp Ser Lys Tyr Ala Tyr Ile Gln Val Thr His Val	1730	1735	1740
Ile Pro Phe Phe Asp Glu Lys Glu Leu Gln Glu Arg Lys Thr Glu Phe	1745	1750	1755
Glu Arg Ser His Asn Ile Arg Arg Phe Met Phe Glu Met Pro Phe Thr	1765	1770	1775
Gln Thr Gly Lys Arg Gln Gly Gly Val Glu Glu Gln Cys Lys Arg Arg	1780	1785	1790
Thr Ile Leu Thr Ala Ile His Cys Phe Pro Tyr Val Lys Lys Arg Ile	1795	1800	1805
Pro Val Met Tyr Gln His His Thr Asp Leu Asn Pro Ile Glu Val Ala	1810	1815	1820
Ile Asp Glu Met Ser Lys Lys Val Ala Glu Leu Arg Gln Leu Cys Ser	1825	1830	1835
Ser Ala Glu Val Asp Met Ile Lys Leu Gln Leu Lys Leu Gln Gly Ser	1845	1850	1855
Val Ser Val Gln Val Asn Ala Gly Pro Leu Ala Tyr Ala Arg Ala Phe	1860	1865	1870
Leu Asp Asp Thr Asn Thr Lys Arg Tyr Pro Asp Asn Lys Val Lys Leu	1875	1880	1885
Leu Lys Glu Val Phe Arg Gln Phe Val Glu Ala Cys Gly Gln Ala Leu	1890	1895	1900
Ala Val Asn Glu Arg Leu Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu	1905	1910	1915
Glu Met Lys Ala Asn Tyr Arg Glu Met Ala Lys Glu Leu Ser Glu Ile	1925	1930	1935
Met His Glu Gln Ile Cys Pro Leu Glu Glu Lys Thr Ser Val Leu Pro	1940	1945	1950
Asn Ser Leu His Ile Phe Asn Ala Ile Ser Gly Thr Pro Thr Ser Thr	1955	1960	1965
Met Val His Gly Met Thr Ser Ser Ser Ser Val Val	1970	1975	1980

<211> 2045

<212> PRT

<213> Homo sapiens

<220>

<223> human CLASP-7

<400> 109

```

Met Ala Ala Ser Glu Arg Arg Ala Phe Ala His Lys Ile Asn Arg Thr
  1             5             10             15

Val Ala Ala Glu Val Arg Lys Gln Val Ser Arg Glu Arg Ser Gly Ser
      20             25             30

Pro His Ser Ser Arg Arg Cys Ser Ser Ser Leu Gly Val Pro Leu Thr
      35             40             45

Glu Val Val Glu Pro Leu Asp Phe Glu Asp Val Leu Leu Ser Arg Pro
      50             55             60

Pro Asp Ala Glu Pro Gly Pro Leu Arg Asp Leu Val Glu Phe Pro Ala
      65             70             75             80

Asp Asp Leu Glu Leu Leu Leu Gln Pro Arg Glu Cys Arg Thr Thr Glu
      85             90             95

Pro Gly Ile Pro Lys Asp Glu Lys Leu Asp Ala Gln Val Arg Ala Ala
      100            105            110

Val Glu Met Tyr Ile Glu Asp Trp Val Ile Val His Arg Arg Tyr Gln
      115            120            125

Tyr Leu Ser Ala Ala Tyr Ser Pro Val Thr Thr Asp Thr Gln Arg Glu
      130            135            140

Arg Gln Lys Gly Leu Pro Arg Gln Val Phe Glu Gln Asp Ala Ser Gly
      145            150            155            160

Asp Glu Arg Ser Gly Pro Glu Asp Ser Asn Asp Ser Arg Arg Gly Ser
      165            170            175

Gly Ser Pro Glu Asp Thr Pro Arg Ser Ser Gly Ala Ser Ser Ile Phe
      180            185            190

Asp Leu Arg Asn Leu Ala Ala Asp Ser Leu Leu Pro Ser Leu Leu Glu
      195            200            205

Arg Ala Ala Pro Glu Asp Val Asp Arg Arg Asn Glu Thr Leu Arg Arg
      210            215            220

Gln His Arg Pro Pro Ala Leu Leu Thr Leu Tyr Pro Ala Pro Asp Glu
      225            230            235            240

Asp Glu Ala Val Glu Arg Cys Ser Arg Pro Glu Pro Pro Arg Glu His
      245            250            255

Phe Gly Gln Arg Ile Leu Val Lys Cys Leu Ser Leu Lys Phe Glu Ile
      260            265            270

Glu Ile Glu Pro Ile Phe Gly Ile Leu Ala Leu Tyr Asp Val Arg Glu
      275            280            285

```

Lys Lys Lys Ile Ser Glu Asn Phe Tyr Phe Asp Leu Asn Ser Asp Ser  
 290 295 300  
 Met Lys Gly Leu Leu Arg Ala His Gly Thr His Pro Ala Ile Ser Thr  
 305 310 315 320  
 Leu Ala Arg Ser Ala Ile Phe Ser Val Thr Tyr Pro Ser Pro Asp Ile  
 325 330 335  
 Phe Leu Val Ile Lys Leu Glu Lys Val Leu Gln Gln Gly Asp Ile Ser  
 340 345 350  
 Glu Cys Cys Glu Pro Tyr Met Val Leu Lys Glu Val Asp Thr Ala Lys  
 355 360 365  
 Asn Lys Glu Lys Leu Glu Lys Leu Arg Leu Ala Ala Glu Gln Phe Cys  
 370 375 380  
 Thr Arg Leu Gly Arg Tyr Arg Met Pro Phe Ala Trp Thr Ala Val His  
 385 390 395 400  
 Leu Ala Asn Ile Val Ser Ser Ala Gly Gln Leu Asp Arg Asp Ser Asp  
 405 410 415  
 Ser Glu Gly Glu Arg Arg Pro Ala Trp Thr Asp Arg Arg Arg Gly  
 420 425 430  
 Pro Gln Asp Arg Ala Ser Ser Gly Asp Asp Ala Cys Ser Phe Ser Gly  
 435 440 445  
 Phe Arg Pro Ala Thr Leu Thr Val Thr Asn Phe Phe Lys Gln Glu Ala  
 450 455 460  
 Glu Arg Leu Ser Asp Glu Asp Leu Phe Lys Phe Leu Ala Asp Met Arg  
 465 470 475 480  
 Arg Pro Ser Ser Leu Leu Arg Arg Leu Arg Pro Val Thr Ala Gln Leu  
 485 490 495  
 Lys Ile Asp Ile Ser Pro Ala Pro Glu Asn Pro His Phe Cys Leu Ser  
 500 505 510  
 Pro Glu Leu Leu His Ile Lys Pro Tyr Pro Asp Pro Arg Gly Arg Pro  
 515 520 525  
 Thr Lys Glu Ile Leu Glu Phe Pro Ala Arg Glu Val Tyr Ala Pro His  
 530 535 540  
 Thr Ser Tyr Arg Asn Leu Leu Tyr Val Tyr Pro His Ser Leu Asn Phe  
 545 550 555 560  
 Ser Ser Arg Gln Gly Ser Val Arg Asn Leu Ala Val Arg Val Gln Tyr  
 565 570 575  
 Met Thr Gly Glu Asp Pro Ser Gln Ala Leu Pro Val Ile Phe Gly Lys  
 580 585 590  
 Ser Ser Cys Ser Glu Phe Thr Arg Glu Ala Phe Thr Pro Val Val Tyr  
 595 600 605



His Asn Lys Ser Pro Glu Phe Tyr Glu Glu Phe Lys Leu His Leu Pro  
 610 615 620  
 Ala Cys Val Thr Glu Asn His His Leu Leu Phe Thr Phe Tyr His Val  
 625 630 635 640  
 Ser Cys Gln Pro Arg Pro Gly Thr Ala Leu Glu Thr Pro Val Gly Phe  
 645 650 655  
 Thr Trp Ile Pro Leu Leu Gln His Gly Arg Leu Arg Thr Gly Pro Phe  
 660 665 670  
 Cys Leu Pro Val Ser Val Asp Gln Pro Pro Pro Ser Tyr Ser Val Leu  
 675 680 685  
 Thr Pro Asp Val Ala Leu Pro Gly Met Arg Trp Val Asp Gly His Lys  
 690 695 700  
 Gly Val Phe Ser Val Glu Leu Thr Ala Val Ser Ser Val His Pro Gln  
 705 710 715 720  
 Asp Pro Tyr Leu Asp Lys Phe Phe Thr Leu Val His Val Leu Glu Glu  
 725 730 735  
 Gly Ala Phe Pro Phe Arg Leu Lys Asp Thr Val Leu Ser Glu Gly Asn  
 740 745 750  
 Val Glu Gln Glu Leu Arg Ala Ser Leu Ala Ala Leu Arg Leu Ala Ser  
 755 760 765  
 Pro Glu Pro Leu Val Ala Phe Ser His His Val Leu Asp Lys Leu Val  
 770 775 780  
 Arg Leu Val Ile Arg Pro Pro Ile Ile Ser Gly Gln Ile Val Asn Leu  
 785 790 795 800  
 Gly Arg Gly Ala Phe Glu Ala Met Ala His Val Val Ser Leu Val His  
 805 810 815  
 Arg Ser Leu Glu Ala Ala Gln Asp Ala Arg Gly His Cys Pro Gln Leu  
 820 825 830  
 Ala Ala Tyr Val His Tyr Ala Phe Arg Leu Pro Gly Thr Glu Pro Ser  
 835 840 845  
 Leu Pro Asp Gly Ala Pro Pro Val Thr Val Gln Ala Ala Thr Leu Ala  
 850 855 860  
 Arg Gly Ser Gly Arg Pro Ala Ser Leu Tyr Leu Ala Arg Ser Lys Ser  
 865 870 875 880  
 Ile Ser Ser Ser Asn Pro Asp Leu Ala Val Ala Pro Gly Ser Val Asp  
 885 890 895  
 Asp Glu Val Ser Arg Ile Leu Ala Ser Lys Leu Leu His Glu Glu Leu  
 900 905 910  
 Ala Leu Gln Trp Val Val Ser Ser Ser Ala Val Arg Glu Ala Ile Leu  
 915 920 925  
 Gln His Ala Trp Phe Phe Phe Gln Leu Met Val Lys Ser Met Ala Leu

930	935	940
His Leu Leu Leu Gly Gln Arg Leu Asp Thr Pro Arg Lys Leu Arg Phe 945 950 955 960		
Pro Gly Arg Phe Leu Asp Asp Ile Thr Ala Leu Val Gly Ser Val Gly 965 970 975		
Leu Glu Val Ile Thr Arg Val His Lys Asp Val Glu Leu Ala Glu His 980 985 990		
Leu Asn Ala Ser Leu Ala Phe Phe Leu Ser Asp Leu Leu Ser Leu Val 995 1000 1005		
Asp Arg Gly Phe Val Phe Ser Leu Val Arg Ala His Tyr Lys Gln Val 1010 1015 1020		
Ala Thr Arg Leu Gln Ser Ser Pro Asn Pro Ala Ala Leu Leu Thr Leu 1025 1030 1035 1040		
Arg Met Glu Phe Thr Arg Ile Leu Cys Ser His Glu His Tyr Val Thr 1045 1050 1055		
Leu Asn Leu Pro Cys Cys Pro Leu Ser Pro Pro Ala Ser Pro Ser Pro 1060 1065 1070		
Ser Val Ser Ser Thr Thr Ser Gln Ser Ser Thr Phe Ser Ser Gln Ala 1075 1080 1085		
Pro Asp Pro Lys Val Thr Ser Met Phe Glu Leu Ser Gly Pro Phe Arg 1090 1095 1100		
Gln Gln His Phe Leu Ala Gly Leu Leu Leu Thr Glu Leu Ala Leu Ala 1105 1110 1115 1120		
Leu Gln Glu Asp Gln Asp Val Arg His Leu Ala Leu Ala Val Leu Lys 1125 1130 1135		
Asn Leu Met Ala Lys His Ser Phe Asp Asp Arg Tyr Arg Glu Pro Arg 1140 1145 1150		
Lys Gln Ala Gln Ile Ala Ser Leu Tyr Met Pro Leu Tyr Gly Met Leu 1155 1160 1165		
Leu Asp Asn Met Pro Arg Ile Arg Leu His Asp Phe Ala Glu Gly Pro 1170 1175 1180		
Gly Gln Arg Ser Arg Leu Ala Ser Met Leu Asp Ser Asp Thr Glu Gly 1185 1190 1195 1200		
Glu Gly Asp Ile Ala Gly Thr Ile Asn Pro Ser Val Ala Met Ala Ile 1205 1210 1215		
Ala Gly Gly Pro Leu Ala Pro Gly Ser Arg Ala Ser Ile Ser Gln Gly 1220 1225 1230		
Pro Pro Thr Ala Ser Arg Ala Gly Cys Ala Leu Ser Ala Glu Ser Ser 1235 1240 1245		
Arg Thr Leu Leu Ala Cys Val Leu Trp Val Leu Lys Asn Thr Glu Pro 1250 1255 1260		

Ala Leu Leu Gln Arg Trp Ala Thr Asp Leu Thr Leu Pro Gln Leu Gly  
 1265 1270 1275 1280  
 Arg Leu Leu Asp Leu Leu Tyr Leu Cys Leu Ala Ala Phe Glu Tyr Lys  
 1285 1290 1295  
 Gly Lys Lys Ala Phe Glu Arg Ile Asn Ser Leu Thr Phe Lys Lys Ser  
 1300 1305 1310  
 Leu Asp Met Lys Ala Arg Leu Glu Glu Ala Ile Leu Gly Thr Ile Gly  
 1315 1320 1325  
 Ala Arg Gln Glu Met Val Arg Arg Ser Arg Glu Arg Ser Pro Phe Gly  
 1330 1335 1340  
 Asn Pro Glu Asn Val Arg Trp Arg Lys Ser Val Thr His Trp Lys Gln  
 1345 1350 1355 1360  
 Thr Ser Asp Arg Val Asp Lys Thr Lys Asp Glu Met Glu His Glu Ala  
 1365 1370 1375  
 Leu Val Glu Gly Asn Leu Ala Thr Glu Ala Ser Leu Val Val Leu Asp  
 1380 1385 1390  
 Thr Leu Glu Ile Ile Val Gln Thr Val Met Leu Ser Glu Ala Arg Glu  
 1395 1400 1405  
 Ser Val Leu Gly Ala Val Leu Lys Val Val Leu Tyr Ser Leu Gly Ser  
 1410 1415 1420  
 Ala Gln Ser Ala Leu Phe Leu Gln His Gly Leu Ala Thr Gln Arg Ala  
 1425 1430 1435 1440  
 Leu Val Ser Lys Phe Pro Glu Leu Leu Phe Glu Glu Asp Thr Glu Leu  
 1445 1450 1455  
 Cys Ala Asp Leu Cys Leu Arg Leu Leu Arg His Cys Gly Ser Arg Ile  
 1460 1465 1470  
 Ser Thr Ile Arg Thr His Ala Ser Ala Ser Leu Tyr Leu Leu Met Arg  
 1475 1480 1485  
 Gln Asn Phe Glu Ile Gly His Asn Phe Ala Arg Val Lys Met Gln Val  
 1490 1495 1500  
 Thr Met Ser Leu Ser Ser Leu Val Gly Thr Thr Gln Asn Phe Ser Glu  
 1505 1510 1515 1520  
 Glu His Leu Arg Arg Ser Leu Lys Thr Ile Leu Thr Tyr Ala Glu Glu  
 1525 1530 1535  
 Asp Met Gly Leu Arg Asp Ser Thr Phe Ala Glu Gln Val Gln Asp Leu  
 1540 1545 1550  
 Met Phe Asn Leu His Met Ile Leu Thr Asp Thr Val Lys Met Lys Glu  
 1555 1560 1565  
 His Gln Glu Asp Pro Glu Met Leu Ile Asp Leu Met Tyr Arg Ile Ala  
 1570 1575 1580

Arg Gly Tyr Gln Gly Ser Pro Asp Leu Arg Leu Thr Trp Leu Gln Asn  
 1585 1590 1595 1600  
 Met Ala Gly Lys His Ala Glu Leu Gly Asn His Ala Glu Ala Ala Gln  
 1605 1610 1615  
 Cys Met Val His Ala Ala Ala Leu Val Ala Glu Tyr Leu Ala Leu Leu  
 1620 1625 1630  
 Glu Asp Gln Arg His Leu Pro Val Gly Cys Val Ser Phe Gln Asn Ile  
 1635 1640 1645  
 Ser Ser Asn Val Leu Glu Glu Ser Ala Ile Ser Asp Asp Ile Leu Ser  
 1650 1655 1660  
 Pro Asp Glu Glu Gly Phe Cys Ser Gly Lys His Phe Thr Glu Leu Gly  
 1665 1670 1675 1680  
 Leu Val Gly Leu Leu Glu Gln Ala Ala Gly Tyr Phe Thr Met Gly Gly  
 1685 1690 1695  
 Leu Tyr Glu Ala Val Asn Glu Val Tyr Lys Asn Leu Ile Pro Ile Leu  
 1700 1705 1710  
 Glu Ala His Arg Asp Tyr Lys Lys Leu Ala Ala Val His Gly Lys Leu  
 1715 1720 1725  
 Gln Glu Ala Phe Thr Lys Ile Met His Gln Ser Ser Gly Trp Glu Arg  
 1730 1735 1740  
 Val Phe Gly Thr Tyr Phe Arg Val Gly Phe Tyr Gly Ala His Phe Gly  
 1745 1750 1755 1760  
 Asp Leu Asp Glu Gln Glu Phe Val Tyr Lys Glu Pro Ser Ile Thr Lys  
 1765 1770 1775  
 Leu Ala Glu Ile Ser His Arg Leu Glu Glu Phe Tyr Thr Glu Arg Phe  
 1780 1785 1790  
 Gly Asp Asp Val Val Glu Ile Ile Lys Asp Ser Tyr Pro Val Asp Lys  
 1795 1800 1805  
 Ser Lys Leu Asp Ser Gln Lys Ala Tyr Ile Gln Ile Thr Tyr Val Glu  
 1810 1815 1820  
 Pro Tyr Phe Asp Thr Tyr Glu Leu Lys Asp Arg Val Thr Tyr Phe Asp  
 1825 1830 1835 1840  
 Arg Asn Tyr Gly Leu Arg Thr Phe Leu Phe Cys Thr Pro Phe Thr Pro  
 1845 1850 1855  
 Asp Gly Arg Ala His Gly Glu Leu Pro Glu Gln His Lys Arg Lys Thr  
 1860 1865 1870  
 Leu Leu Ser Thr Asp His Ala Phe Pro Tyr Ile Lys Thr Arg Ile Arg  
 1875 1880 1885  
 Val Cys His Arg Glu Glu Thr Val Leu Thr Pro Val Glu Val Ala Ile  
 1890 1895 1900  
 Glu Asp Met Gln Lys Lys Thr Arg Glu Leu Ala Phe Ala Thr Glu Gln

1905                      1910                      1915                      1920  
 Asp Pro Pro Asp Ala Lys Met Leu Gln Met Val Leu Gln Gly Ser Val  
                                  1925                      1930                      1935  
 Gly Pro Thr Val Asn Gln Gly Pro Leu Glu Val Ala Gln Val Phe Leu  
                                  1940                      1945                      1950  
 Ala Glu Ile Pro Glu Asp Pro Lys Leu Phe Arg His His Asn Lys Leu  
                                  1955                      1960                      1965  
 Arg Leu Cys Phe Lys Asp Phe Cys Lys Lys Cys Glu Asp Ala Leu Arg  
                                  1970                      1975                      1980  
 Lys Asn Lys Ala Leu Ile Gly Pro Asp Gln Lys Glu Tyr His Arg Glu  
 1985                                   1990                      1995                      2000  
 Leu Glu Arg Asn Tyr Cys Arg Leu Arg Glu Ala Leu Gln Pro Leu Leu  
                                  2005                      2010                      2015  
 Thr Gln Arg Leu Pro Gln Leu Met Ala Pro Thr Pro Pro Gly Leu Arg  
                                  2020                      2025                      2030  
 Asn Ser Leu Asn Arg Ala Ser Phe Arg Lys Ala Asp Leu  
                                  2035                      2040                      2045  
  
 <210> 110  
 <211> 2180  
 <212> PRT  
 <213> Homo sapiens  
  
 <220>  
 <223> human CLASP-1  
  
 <400> 110  
 Met Ser Phe Arg Gly Lys Val Phe Lys Arg Glu Pro Ser Glu Phe Trp  
   1                                  5                                  10                                  15  
 Lys Lys Arg Arg Thr Val Arg Arg Val Ile Gln Glu Glu Phe His Arg  
                                   20                                  25                                  30  
 Phe Ser Ser Gln Glu Lys Pro Arg Leu Leu Glu Pro Leu Asp Tyr Glu  
                                   35                                  40                                  45  
 Thr Val Ile Glu Glu Leu Glu Lys Thr Tyr Arg Asn Asp Pro Leu Gln  
   50                                  55                                  60  
 Asp Leu Leu Phe Phe Pro Ser Asp Asp Phe Ser Ala Ala Thr Val Ser  
   65                                  70                                  75                                  80  
 Trp Asp Ile Arg Thr Leu Tyr Ser Thr Val Pro Glu Asp Ala Glu His  
                                   85                                  90                                  95  
 Lys Ala Glu Asn Leu Leu Val Lys Glu Ala Cys Lys Phe Tyr Ser Ser  
                                   100                                  105                                  110  
 Gln Trp His Val Val Asn Tyr Lys Tyr Glu Gln Tyr Ser Gly Asp Ile  
                                   115                                  120                                  125  
 Arg Gln Leu Pro Arg Ala Glu Tyr Lys Pro Glu Lys Leu Pro Ser His

130	135	140
Ser Phe Glu Ile Asp His Glu Asp Ala Asp Lys Asp Glu Asp Thr Thr		
145	150	155 160
Ser His Ser Ser Ser Lys Gly Gly Gly Gly Ala Gly Gly Thr Gly Val		
	165	170 175
Phe Lys Ser Gly Trp Leu Tyr Lys Gly Asn Phe Asn Ser Thr Val Asn		
	180	185 190
Asn Thr Val Thr Val Arg Ser Phe Lys Lys Arg Tyr Phe Gln Leu Thr		
	195	200 205
Gln Leu Pro Asp Asn Ser Tyr Ile Met Asn Phe Tyr Lys Asp Glu Lys		
	210	215 220
Ile Ser Lys Glu Pro Lys Gly Cys Ile Phe Leu Asp Ser Cys Thr Gly		
	225	230 235 240
Val Val Gln Asn Asn Arg Leu Arg Lys Tyr Ala Phe Glu Leu Lys Met		
	245	250 255
Asn Asp Leu Thr Tyr Phe Val Leu Ala Ala Glu Thr Glu Ser Asp Met		
	260	265 270
Asp Glu Trp Ile His Thr Leu Asn Arg Ile Leu Gln Ile Ser Pro Glu		
	275	280 285
Gly Pro Leu Gln Gly Arg Arg Ser Thr Glu Leu Thr Asp Leu Gly Leu		
	290	295 300
Asp Ser Leu Asp Asn Ser Val Thr Cys Glu Cys Thr Pro Glu Glu Thr		
	305	310 315 320
Asp Ser Ser Glu Asn Asn Leu His Ala Asp Phe Ala Lys Tyr Leu Thr		
	325	330 335
Glu Thr Glu Asp Thr Val Lys Thr Thr Arg Asn Met Glu Arg Leu Asn		
	340	345 350
Leu Phe Ser Leu Asp Pro Asp Ile Asp Thr Leu Lys Leu Gln Lys Lys		
	355	360 365
Asp Leu Leu Glu Pro Glu Ser Val Ile Lys Pro Phe Glu Glu Lys Ala		
	370	375 380
Ala Lys Arg Ile Met Ile Ile Cys Lys Ala Leu Asn Ser Asn Leu Gln		
	385	390 395 400
Gly Cys Val Thr Glu Asn Glu Asn Asp Pro Ile Thr Asn Ile Glu Pro		
	405	410 415
Phe Phe Val Ser Val Ala Leu Tyr Asp Leu Arg Asp Ser Arg Lys Ile		
	420	425 430
Ser Ala Asp Phe His Val Asp Leu Asn His Ala Ala Val Arg Gln Met		
	435	440 445
Leu Leu Gly Ala Ser Val Ala Leu Glu Asn Gly Asn Ile Asp Thr Ile		
	450	455 460

Thr Pro Arg Gln Ser Glu Glu Pro His Ile Lys Gly Leu Pro Glu Glu  
 465 470 475 480  
 Trp Leu Lys Phe Pro Lys Gln Ala Val Phe Ser Val Ser Asn Pro His  
 485 490 495  
 Ser Glu Ile Val Leu Val Ala Lys Ile Glu Lys Val Leu Met Gly Asn  
 500 505 510  
 Ile Ala Ser Gly Ala Glu Pro Tyr Ile Lys Asn Pro Asp Ser Asn Lys  
 515 520 525  
 Tyr Ala Gln Lys Ile Leu Lys Ser Asn Arg Gln Phe Cys Ser Lys Leu  
 530 535 540  
 Gly Lys Tyr Arg Arg Ala Phe Ala Trp Ala Val Arg Ser Val Phe Lys  
 545 550 555 560  
 Asp Asn Gln Gly Asn Val Asp Arg Asp Ser Arg Phe Ser Pro Leu Phe  
 565 570 575  
 Arg Gln Glu Ser Ser Lys Ile Ser Thr Glu Asp Leu Val Lys Leu Val  
 580 585 590  
 Ser Asp Tyr Arg Arg Ala Asp Arg Ile Ser Lys Met Gln Thr Ile Pro  
 595 600 605  
 Gly Ser Leu Asp Ile Ala Val Asp Asn Val Pro Leu Glu His Pro Asn  
 610 615 620  
 Cys Val Thr Ser Ser Phe Ile Pro Val Lys Pro Phe Asn Met Met Ala  
 625 630 635 640  
 Gln Thr Glu Pro Thr Val Glu Val Glu Glu Phe Val Tyr Asp Ser Thr  
 645 650 655  
 Lys Tyr Cys Arg Pro Tyr Arg Val Tyr Lys Asn Gln Ile Tyr Ile Tyr  
 660 665 670  
 Pro Lys His Leu Lys Tyr Asp Ser Gln Lys Cys Phe Asn Lys Ala Arg  
 675 680 685  
 Asn Ile Thr Val Cys Ile Glu Phe Lys Asn Ser Asp Glu Glu Ser Ala  
 690 695 700  
 Lys Pro Leu Lys Cys Ile Tyr Gly Lys Pro Glu Gly Pro Leu Phe Thr  
 705 710 715 720  
 Ser Ala Ala Tyr Thr Ala Val Leu His His Ser Gln Asn Pro Asp Phe  
 725 730 735  
 Ser Asp Glu Val Lys Ile Glu Leu Pro Thr Gln Leu His Glu Lys His  
 740 745 750  
 His Ile Leu Phe Ser Phe Tyr His Val Thr Cys Asp Ile Asn Ala Lys  
 755 760 765  
 Ala Asn Ala Lys Lys Lys Glu Ala Leu Glu Thr Ser Val Gly Tyr Ala  
 770 775 780

Trp Leu Pro Leu Met Lys His Asp Gln Ile Ala Ser Gln Glu Tyr Asn  
 785 790 795 800  
 Ile Pro Ile Ala Thr Ser Leu Pro Pro Asn Tyr Leu Ser Phe Gln Asp  
 805 810 815  
 Ser Ala Ser Gly Lys His Gly Gly Ser Asp Ile Lys Trp Val Asp Gly  
 820 825 830  
 Gly Lys Pro Leu Phe Lys Val Ser Thr Phe Val Val Ser Thr Val Asn  
 835 840 845  
 Thr Gln Asp Pro His Val Asn Ala Phe Phe Gln Glu Cys Gln Lys Arg  
 850 855 860  
 Glu Lys Asp Met Ser Gln Ser Pro Thr Ser Asn Phe Ile Arg Ser Cys  
 865 870 875 880  
 Lys Asn Leu Leu Asn Val Glu Lys Ile His Ala Ile Met Ser Phe Leu  
 885 890 895  
 Pro Ile Ile Leu Asn Gln Leu Phe Lys Val Leu Val Gln Asn Glu Glu  
 900 905 910  
 Asp Glu Ile Thr Thr Thr Val Thr Arg Val Leu Pro Asp Ile Val Ala  
 915 920 925  
 Lys Cys His Glu Glu Gln Leu Asp His Ser Val Gln Ser Tyr Ile Lys  
 930 935 940  
 Phe Val Phe Lys Thr Arg Ala Cys Lys Glu Arg Pro Val His Glu Asp  
 945 950 955 960  
 Leu Ala Lys Asn Val Thr Gly Leu Leu Lys Ser Asn Asp Ser Pro Thr  
 965 970 975  
 Val Lys His Val Leu Lys His Ser Trp Phe Phe Phe Ala Ile Ile Leu  
 980 985 990  
 Lys Ser Met Ala Gln His Leu Ile Asp Thr Asn Lys Ile Gln Leu Pro  
 995 1000 1005  
 Arg Pro Gln Arg Phe Pro Glu Ser Tyr Gln Asn Glu Leu Asp Asn Leu  
 1010 1015 1020  
 Val Met Val Leu Ser Asp His Val Ile Trp Lys Tyr Lys Asp Ala Leu  
 1025 1030 1035 1040  
 Glu Glu Thr Arg Arg Ala Thr His Ser Val Ala Arg Phe Leu Lys Arg  
 1045 1050 1055  
 Cys Phe Thr Phe Met Asp Arg Gly Cys Val Phe Lys Met Val Asn Asn  
 1060 1065 1070  
 Tyr Ile Ser Met Phe Ser Ser Gly Asp Leu Lys Thr Leu Cys Gln Tyr  
 1075 1080 1085  
 Lys Phe Asp Phe Leu Gln Glu Val Cys Gln His Glu His Phe Ile Pro  
 1090 1095 1100  
 Leu Cys Leu Pro Ile Arg Ser Ala Asn Ile Pro Asp Pro Leu Thr Pro



1105	1110	1115	1120
Ser Glu Ser Thr Gln Glu Leu His Ala Ser Asp Met Pro Glu Tyr Ser			
1125	1130	1135	
Val Thr Asn Glu Phe Cys Arg Lys His Phe Leu Ile Gly Ile Leu Leu			
1140	1145	1150	
Arg Glu Val Gly Phe Ala Leu Gln Glu Asp Gln Asp Val Arg His Leu			
1155	1160	1165	
Ala Leu Ala Val Leu Lys Asn Leu Met Ala Lys His Ser Phe Asp Asp			
1170	1175	1180	
Arg Tyr Arg Glu Pro Arg Lys Gln Ala Gln Ile Ala Ser Leu Tyr Met			
1185	1190	1195	1200
Pro Leu Tyr Gly Met Leu Leu Asp Asn Met Pro Arg Ile Tyr Leu Lys			
1205	1210	1215	
Asp Leu Tyr Pro Phe Thr Val Asn Thr Ser Asn Gln Gly Ser Arg Asp			
1220	1225	1230	
Asp Leu Ser Thr Asn Gly Gly Phe Gln Ser Gln Thr Ala Ile Lys His			
1235	1240	1245	
Ala Asn Ser Val Asp Thr Ser Phe Ser Lys Asp Val Leu Asn Ser Ile			
1250	1255	1260	
Ala Ala Phe Ser Ser Ile Ala Ile Ser Thr Val Asn His Ala Asp Ser			
1265	1270	1275	1280
Arg Ala Ser Leu Ala Ser Leu Asp Ser Asn Pro Ser Thr Asn Glu Lys			
1285	1290	1295	
Ser Ser Glu Lys Thr Asp Asn Cys Glu Lys Ile Pro Arg Pro Leu Ala			
1300	1305	1310	
Leu Ile Gly Ser Thr Leu Arg Phe Asp Arg Leu Asp Gln Ala Glu Thr			
1315	1320	1325	
Arg Ser Leu Leu Met Cys Phe Leu His Ile Met Lys Thr Ile Ser Tyr			
1330	1335	1340	
Glu Thr Leu Ile Ala Tyr Trp Gln Arg Ala Pro Ser Pro Glu Val Ser			
1345	1350	1355	1360
Asp Phe Phe Ser Ile Leu Asp Val Cys Leu Gln Asn Phe Arg Tyr Leu			
1365	1370	1375	
Gly Lys Arg Asn Ile Ile Arg Lys Ile Ala Ala Ala Phe Lys Phe Val			
1380	1385	1390	
Gln Ser Thr Gln Asn Asn Gly Thr Leu Lys Gly Ser Asn Pro Ser Cys			
1395	1400	1405	
Gln Thr Ser Gly Leu Leu Ala Gln Trp Met His Ser Thr Ser Arg His			
1410	1415	1420	
Glu Gly His Lys Gln His Arg Ser Gln Thr Leu Pro Ile Ile Arg Gly			
1425	1430	1435	1440

Lys Asn Ala Leu Ser Asn Pro Lys Leu Leu Gln Met Leu Asp Asn Thr  
 1445 1450 1455  
 Met Thr Ser Asn Ser Asn Glu Ile Asp Ile Val His His Val Asp Thr  
 1460 1465 1470  
 Glu Ala Asn Ile Ala Thr Glu Gly Cys Leu Thr Ile Leu Asp Leu Val  
 1475 1480 1485  
 Ser Leu Phe Thr Gln Thr His Gln Arg Gln Leu Gln Gln Cys Asp Cys  
 1490 1495 1500  
 Gln Asn Ser Leu Met Lys Arg Gly Phe Asp Thr Tyr Met Leu Phe Phe  
 1505 1510 1515 1520  
 Gln Val Asn Gln Ser Ala Thr Ala Leu Lys His Val Phe Ala Ser Leu  
 1525 1530 1535  
 Arg Leu Phe Val Cys Lys Phe Pro Ser Ala Phe Phe Gln Gly Pro Ala  
 1540 1545 1550  
 Asp Leu Cys Gly Ser Phe Cys Tyr Glu Val Leu Lys Cys Cys Asn His  
 1555 1560 1565  
 Arg Ser Arg Ser Thr Gln Thr Glu Ala Ser Ala Leu Leu Tyr Leu Phe  
 1570 1575 1580  
 Met Arg Lys Asn Phe Glu Phe Asn Lys Gln Lys Ser Ile Val Arg Ser  
 1585 1590 1595 1600  
 His Leu Gln Leu Ile Lys Ala Val Ser Gln Leu Ile Ala Asp Ala Gly  
 1605 1610 1615  
 Ile Gly Gly Ser Arg Phe Gln His Ser Leu Ala Ile Thr Asn Asn Phe  
 1620 1625 1630  
 Ala Asn Gly Asp Lys Gln Met Lys Asn Ser Asn Phe Pro Ala Glu Val  
 1635 1640 1645  
 Lys Asp Leu Thr Lys Arg Ile Arg Thr Val Leu Met Ala Thr Ala Gln  
 1650 1655 1660  
 Met Lys Glu His Glu Lys Asp Pro Glu Met Leu Val Asp Leu Gln Tyr  
 1665 1670 1675 1680  
 Ser Leu Ala Asn Ser Tyr Ala Ser Thr Pro Glu Leu Arg Arg Thr Trp  
 1685 1690 1695  
 Leu Glu Ser Met Ala Lys Ile His Ala Arg Asn Gly Asp Leu Ser Glu  
 1700 1705 1710  
 Ala Ala Met Cys Tyr Ile His Ile Ala Ala Leu Ile Ala Glu Tyr Leu  
 1715 1720 1725  
 Lys Arg Lys Gly Tyr Trp Lys Val Glu Lys Ile Cys Thr Ala Ser Leu  
 1730 1735 1740  
 Leu Ser Glu Asp Thr His Pro Cys Asp Ser Asn Ser Leu Leu Thr Thr  
 1745 1750 1755 1760

Pro Ser Gly Gly Ser Met Phe Ser Met Gly Trp Pro Ala Phe Leu Ser  
 1765 1770 1775  
 Ile Thr Pro Asn Ile Lys Glu Glu Gly Ala Ala Lys Glu Asp Ser Gly  
 1780 1785 1790  
 Met His Asp Thr Pro Tyr Asn Glu Asn Ile Leu Val Glu Gln Leu Tyr  
 1795 1800 1805  
 Met Cys Gly Glu Phe Leu Trp Lys Ser Glu Arg Tyr Glu Leu Ile Ala  
 1810 1815 1820  
 Asp Val Asn Lys Pro Ile Ile Ala Val Phe Glu Lys Gln Arg Asp Phe  
 1825 1830 1835 1840  
 Lys Lys Leu Ser Asp Leu Tyr Tyr Asp Ile His Arg Ser Tyr Leu Lys  
 1845 1850 1855  
 Val Ala Glu Val Val Asn Ser Glu Lys Arg Leu Phe Gly Arg Tyr Tyr  
 1860 1865 1870  
 Arg Val Ala Phe Tyr Gly Gln Gly Phe Phe Glu Glu Glu Glu Gly Lys  
 1875 1880 1885  
 Glu Tyr Ile Tyr Lys Glu Pro Lys Leu Thr Gly Leu Ser Glu Ile Ser  
 1890 1895 1900  
 Gln Arg Leu Leu Lys Leu Tyr Ala Asp Lys Phe Gly Ala Asp Asn Val  
 1905 1910 1915 1920  
 Lys Ile Ile Gln Asp Ser Asn Lys Val Asn Pro Lys Asp Leu Asp Pro  
 1925 1930 1935  
 Lys Tyr Ala Tyr Ile Gln Val Thr Tyr Val Thr Pro Phe Phe Glu Glu  
 1940 1945 1950  
 Lys Glu Ile Glu Asp Arg Lys Thr Asp Phe Glu Met His His Asn Ile  
 1955 1960 1965  
 Asn Arg Phe Val Phe Glu Thr Pro Phe Thr Leu Ser Gly Lys Lys His  
 1970 1975 1980  
 Gly Gly Val Ala Glu Gln Cys Lys Arg Arg Thr Ile Leu Thr Thr Ser  
 1985 1990 1995 2000  
 His Leu Phe Pro Tyr Val Lys Lys Arg Ile Gln Val Ile Ser Gln Ser  
 2005 2010 2015  
 Ser Thr Glu Leu Asn Pro Ile Glu Val Ala Ile Asp Glu Met Ser Arg  
 2020 2025 2030  
 Lys Val Ser Glu Leu Asn Gln Leu Cys Thr Met Glu Glu Val Asp Met  
 2035 2040 2045  
 Ile Ser Leu Gln Leu Lys Leu Gln Gly Ser Val Ser Val Lys Val Asn  
 2050 2055 2060  
 Ala Gly Pro Met Ala Tyr Ala Arg Ala Phe Leu Glu Glu Thr Asn Ala  
 2065 2070 2075 2080  
 Lys Lys Tyr Pro Asp Asn Gln Val Lys Leu Leu Lys Glu Ile Phe Arg

2085	2090	2095
Gln Phe Ala Asp Ala Cys Gly Gln Ala Leu Asp Val Asn Glu Arg Leu 2100	2105	2110
Ile Lys Glu Asp Gln Leu Glu Tyr Gln Glu Glu Leu Arg Ser His Tyr 2115	2120	2125
Lys Asp Met Leu Ser Glu Leu Ser Thr Val Met Asn Glu Gln Ile Thr 2130	2135	2140
Gly Arg Asp Asp Leu Ser Lys Arg Gly Val Asp Gln Thr Cys Thr Arg 2145	2150	2155 2160
Val Ile Ser Lys Ala Thr Pro Ala Leu Pro Thr Val Ser Ile Ser Ser 2165	2170	2175
Ser Ala Glu Val 2180		

<210> 111  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:oligo 1

<400> 111  
 cccccaagac gctctccccg gcttctgaaa g

31

<210> 112  
 <211> 31  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:oligo 2

<400> 112  
 ccgcgtgcac catgcactgg gcggcctcgg c

31

<210> 113  
 <211> 34  
 <212> DNA  
 <213> Artificial Sequence

<220>  
 <223> Description of Artificial Sequence:oligo 3

<400> 113  
 ggccagctcc cgtgtcttct tctgcatgtc ctcg

34

<210> 114  
 <211> 19  
 <212> DNA  
 <213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:sense  
oligonucleotide C7gS23

<400> 114  
ctggactttg aggatgtac

19

<210> 115  
<211> 21  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> Description of Artificial Sequence:antisense  
oligonucleotide C7AS16

<400> 115  
agggtgaaga atttgtccag g

21

B1  
Cont

